166996160

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GenCore version 5.1.6
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OM protein - protein search, using sw mode;

September 27, 2003, C6:45:13 : Search Lime 23 Seconds (without aliquments) 372:124 Million cell updates/sec Run on:

US-09-965-594-1 953 Title: Perfect score: Sequence:

1 MAPITAYAQQIRGLLGCIIT......SVAKAVDFIPVESLETTMRS 182 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 99% Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description		h genome	h genome	c	۲.	æ	л	P26660 h genome po	ä,				ara							retha	P51124 homo sapien	mus m	mus m		C03131 saccharopol				cps		P18614 rattus nerv		hepa
SOMMAKIES	ID	POLG_HCV1	POLG_HCVH	POLG_HCVTW	POLG_HCVBK	POLG_HCV.JA	POLG_HCVJI	POLG_HCVJ8	POLG_HCVJ6	PAAD_PSEAE	HHOA_ARATH	AAMP_HUMAN	Y136_TREPA	DEG1_ARATH	CAC3_BOVIN	ZP3_RABII	HYPF_AZOVI	TB11_NEIMB	PANE_RHILO	GRAK_MOUSE	HELS_METMA	GRAM_HUMAN	SAD1_MOUSE	CA1H_MOUSE	CENE_HUMAN	ERY1_SACER	GRAD_MOUSE	VPRT_SMRVH	SPR1_IPOBA	UL16_EBV	PGL2_RALSO	ITA1_RAT	CTRL_HUMAN	VST2_HEVME
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2 homo sapien	4 human cytom	5 human cytom	3 oryctolagus	9 methanosarc	6 neisseria g	4 schizosacch	6 brucella me	9 bacillus th	0 bacillus th	0 homo sapien	1 homo sapien
P1953	P0643	P0643	P2886	08t13	001996	P3243	OBye7	P0551	P1648	P9816	P0831
TFE3_HUMAN	VIE3_HCMVT	VIE2_HCMVT	MM03_RABIT	HELS_METAC	TBP1_NEIGO	CWG2_SCHPO	DNAK_BRUME	C4BA_BACTI	C4AA_BACTI	PGBM_HUMAN	CATG_HUMAN
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S	70	20	70	7.0	69.5	69	69	69	69	69	68.5
70.											

## ALIGNMENTS

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CELLULAR AMINOPEFILDASE.
CAPESD PROTEIN C (POTENTIAL).
MAJOR ENVELOPE PROTEIN S (POTENTIAL).
MAJOR ENVELOPE PROTEIN S (POTENTIAL).
NONSTRUCTURAL PROTEIN NS; (POTENTIAL).
PROTEASE/HELICASE NS3 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS24 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS44 (POTENTIAL).
RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
                                                                                                                                                                                                                                                        Polyprotein; Clycoprotein; Iransferase; RNA-directed RNA polymerase; Core protein; Coat protein; Envelope protein; Helicase; ATP-binding; Transmembrane; Nonstructural protein; Hydrolase; Serine protease;
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RNA_pol_DS_PS.
RNA_pol_PSvir.
                                                                                                                                                   Pfam; PF01560; HCV_NG1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF012907; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4s; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5s; 1.
Pfam; PF00271; helicasc_C; 1.
Pfam; PF00988; Viral_RGRP; 1.
PF0Dom; PF00998; Viral_RGRP; 1.
                                                  HCV_NS4a.
HCV_NS4b.
HCV_NS5a.
                                                                                 HCV_RdRP.
                               HCV_NS2.
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PF01542; HCV_core; 1
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                    InterPro; 1PR002531; F
InterPro; 1PR002518; F
InterPro; 1PR004109; I
InterPro; 1PR00415; F
                                                                                                    InterPro: IPR007095;
InterPro: IPR007094;
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Query Match 99.0%; Score 943; DB 1; Length 3011;
Best Local Similarity 98.4%; Pred. No. 3.4e-82;
Matches 179; Conservative 3; Mismatches 0; Indels 0; Gaps

1 MAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGA 60

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(1-406-1992 (Rel. 23, Created)
(1-406-1992 (Rel. 23, Last sequence update)
(1-5-2003 (Rel. 42, Last annotation update)
(15-52P-2003 (Rel. 42, Last annotation update)
(GP68) (GP06) (NSI); Protein PT (GP83) (GP35); Envelope glycoprotein E2
(GF68) (GP70) (NSI); Protein PT; Nonstructural protein NS2 (P21)
(EC 3.4.29.-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein NS5A (P56); Nonstructural protein NS5A (P56); Nonstructural protein NS5A (P60) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48);
(Epacitis C virus (isolate H) (HCV) X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1192-1657.
MEDLINE-9816321: PubMed-9493270;
Kim J.L., Morgenstern K.A., Griffith J.P., Dwyer M.D., Thomson J.A.,
Murcko M.A., Lin C., Caron P.R.;
"Hepatitis C virus NS3 RNA helicase domain with a bound
oligonucleotide: the crystal structure provides insights into the mode
of unwinding."; Weber P.C.; GIRTIASPKSPVIOMYTNVDKDLVGWPAPQGSRSLIPCTCGSSDLYLVTRHADVIPVRRR -!- FUNCTION: PROTEASE NS2 IS RESPONSIBLE FOR THE CLEAVAGE OF NS2-NS3-FUNCTION: PROTEASE NS3 IS RESPONSIBLE FOR THE CLEAVAGE OF NS3-NS3-NS4A, NS4A-NS4B, NS4B-NS5A-NS5A-NS5B.
-!- FUNCTION: NS4A FORMS A COMPLEX WITH NS3 AND IS ESSENTIAL FOR THE in the viral {RNA}{N}.
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: E1 AND E2. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA. -:- FUNCTION: NSSA SEEMS TO HAVE A TRANSCRIPTIONAL ACTIVATORY ROLE.
-:- FUNCTION: NSSB IS A RNA-DEPENDENT RNA POLYMERASE THAT PLAYS AN
ESSENTIAL ROLE IN THE VIRUS REPLICATION.
-:- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the vira
precursor polyprotein, commonly with Asp or Glu in the P6
position, Cys or Thr in P1 and Ser or Ala in P1'.
-:- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + U "Genomic structure of the human prototype strain H of hepatitis virus: comparison with American and Japanese isolates."; Proc. Natl. Acad. Sci. U.S.A. 88:10292-10296(1991). MEDLINE-92052256; PubMed-1658800; Inchauspe G., Zebedee S., Lee D.H.H., Sugitani M., Nasoff M., Prince A.M.; X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 1207-1657.
MEDLINE-97331322; PubMed-9187654;
MARO N., Hesson T., Cable M., Hong Z., Kwong A.D., Lc H.V.,
"Structure of the hepatitis C virus RNA holicase domain.";
Nat. Struct. Biol. 4:463-467(1997). PRT; 3011 AA STANDARD; Structure 6:89-100(1998) NS3. SEQUENCE FROM N.A. ACTIVATION OF NCBI\_TaxID=11108; RS 1207 182 RS Hepacivirus POLG\_HCVH ID POLG\_HCVH AC P27958; 18. 61 RESULT 8 3 ó a ð a 

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Pred. No. 1.2e-80;
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    This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Gage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polyprotein; Glycoprotein; Transferase; RNA-directed KNA polymerase;
Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
Transmembrane; Nonstructural protein; Hydrolase; Serine protease;
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SIMILARITY).
SIMILARITY).
PTM: THE STRUCTURAL PROTEINS C, EL AND E2 ARE PRODUCED BY PROTECLYTTO PROCESSING BY THE HOST SIGNAL PEPTIDAGESS.
SIMILARITY: THE NS2 PROTEGASE BELONGS TO PETIDAGE FAMILY U39. SIMILARITY: THE NS3 PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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CELLULAR ANINGPERTIDASE:
CAPSID PROTEIN C.
ENVELOPE GLYCOPROTEIN EI.
ENVELOPE GLYCOPROTEIN EI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEASE/HELICASE NG3.
NONSTRUCTURAL PROTEIN NA4A.
NONSTRUCTURAL PROTEIN NA4B.
NONSTRUCTURAL PROTEIN NS5B.
NONSTRUCTURAL PROTEIN NS5B.
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NONSTRUCTURAL PROTEIN NS2.
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CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
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DECH BOX.
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MEROPS: U39:001: -
TRANSFAC: TC4155: -
InterPro: IPRG0141C; DEAD.
InterPro: IPRG0141C; DEAD.
InterPro: IPRG02521; HCV_core.
InterPro: IPRG02521; HCV_core.
InterPro: IPRG02513; HCV_core.
InterPro: IPRG02513; HCV_NS1.
InterPro: IPRG02518; HCV_NS2.
InterPro: IPRG02518; HCV_NS2.
InterPro: IPRG02518; HCV_NS3.
InterPro: IPRG02618; HCV_NS3.
InterPro: IPRG01490; HCV_NS3.
InterPro: IPRG01490; HCV_NS4.
InterPro: IPRG0166; HCV_NS5a.
InterPro: IPRG0166; HCV_NS5a.
InterPro: IPRG0166; HCV_NS5a.
InterPro: IPRG0166; HCV_NS5a.
InterPro: IPRG0169; HNA_pol_PSvir.
Pfam: PFG1542; HCV_NS2; I.
Pfam: PFG1558; HCV_NS2; I.
Pfam: PFG1558; HCV_NS3; I.
Pfam: PFG1560; HCV_NS3; I.
Pfam: PFG1060; HCV_NS4; I.
Pfam: PFG0160; HCV_NS4; I.
Pfam: PFG0160; HCV_NS4; I.
Pfam: PFG0160; HCV_NS4; I.
Pfam: PFG0160; HCV_NS5a; I.
                                                                                                                                                                                                 EMBL, M67463, AA45534.1; -. PIR, A36814; GWNVCH. PDB; 1HE! 25.NOV-98. PDB; 1A1V: 16-FEB-99. PDB; 1A1V: 16-FEB-99.
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                                 121 GDSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTM 180
                                                                                                                                                                                                                                                                                                                                                                                                             01-APR.1993 (Rel. 25, Created)
01-APR.1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last aenoctation update)
6enome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
(GP68) (GP70) (NG1); Protein P7: Nonstructural protein NS2 (P21)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepcarivin)
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P66) (P70) (NRA-directed RNA polymerase) (EC 2.7.7.48));
Hepatitis C virus (isolate Taiwan) (HCV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTRIIASPKGPVIQMYTNVDKDLVGWPAPQGSRSLIPCIGGSSDLYLVTRHADVIPVRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLESCAPSID COVERED BY A LIPOPROPERIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GIYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
   s: Indels
   4; Mismatches
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Matches 175; Conservative
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PDB; lN64; 25-FEB-03.
PDB; lNS3; 08-APR-98.
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P29846;
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CELLULAR AMINOPEPTIDASE.
CORE PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NSI/EZ (POTENTIAL).
PROTEASE/HELICASE NSI (POTENTIAL).
NONSTRUCTURAL PROTEIN NSIA (POTENTIAL).
NONSTRUCTURAL PROTEIN NSIA (POTENTIAL).
NONSTRUCTURAL PROTEIN NSIA (POTENTIAL).
RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase; Core protein; Coat protein; Envelope protein; Helicase; ATP-binding; Transmembrane; Nonstructural protein; Hydrolase; Serlne protease;
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CHARGE RELAY SYSTEM (BY SIMILARITY)
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DECH BOX.
N-LINKED (GLCNAC.
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                                                                  IPRC02868; HCV_NS5a.
IPRO02166; HCV_RGRP.
IPRO07095; RNA_POl_DS_PS.
IPRO07094; RNA_POl_PSvir.
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HCV_NS3.
HCV_NS4a.
HCV_NS4b.
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Pfam: PF01001; HCV_NS4b: 1.
Pfam: PF01505; HCV_NS5a: 1.
Pfam: PF00271; helicase_C: 1.
Pfam: PF00998; Viral_RGRP: 1.
ProDom; PD186062: HCV_NS1; 1.
                                                                                                                                                     Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_env; 1.
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HCV_NS2; 1.
HCV_NS3; 1.
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IPR004109; H
IPR000745; H
IPR001490; H
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Best Local Similarity
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 121 GDSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTM 189
                                                                 61 GTRTIASPKGPVIQMYTNVDKDLVGWPAFQGSRSLTFGTGGSSDLYLVTRHADV!PVRRR 120
MAPITAYAQQTRGLLGCTITSLTGRBKNQVEGEVQ1VSTAAQTFLATCINGVCWTVYHGA 63
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDDLINE=91140656; PubMed=1847440;
Takamizawa A., Mori C., Fuke I., Manabe S., Murakami S., Fujita J.,
Takamizawa A., Mori C., Puke I., Okayama H.;
"Structure and organization of the hepatitis C virus genome isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Love R.A., Parge H.E., Wickersham J.A., Hostomsky Z., Habuka N., Moomaw E.W., Adachi T., Hostomska Z.; Moomaw E.W., The crystal structure of hepatitis C virus NS3 proteinase reveals trypsin-like fold and a structural zinc binding site."; Cell 87:331-342(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1027-1210 AND 1678-1691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borowski P., Heiland M., Ochimann K., Becker B., Korneteky L.
"Non-structural protein 3 of hepatitis C virus inhibits
phosphorylation mediated by CAMP-dependent protein kinase.";
Bur. J. Blochem. 237:611-618(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1627-1215.
MEDLINE=97015088: PubMed=8861916;
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J. Virol. 65:1105-1113(1991).
                                                                                                                                                                                                                                                                                                          STANDARD;
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NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

RNA-DIRECTED RNA POLIMERASE (POTENTIAL).
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN BYNYELOPE. THE ENVELOPE CONSISIS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMARI; SM00487; DEXDC: 1.
POLIPPOLOEIN: GLYCOPTOCEIN: Transferase; RNA-directed kNA polymerase; Core protein; Gaat protein: Envelope protein; Helicase; ATP-binding; Transmembrane; Nonstructural protein; Hydrolase; Serine protease:
                                                                                                                 SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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Interpro; IPR001410; DEAD.
Interpro; IPR001522; HCV_capsid.
Interpro; IPR002521; HCV_core.
Interpro; IPR002513; HCV_core.
Interpro; IPR002513; HCV_NS1.
Interpro; IPR001490; HCV_NS2.
Interpro; IPR001490; HCV_NS4.
Interpro; IPR001490; HCV_NS4.
Interpro; IPR001490; HCV_NS4.
Interpro; IPR001490; HCV_NS4.
Interpro; IPR001964; HCV_NS4.
Interpro; IPR001964; RNA_POL_PSP.
Interpro; IPR001994; HCV_core: I.
Pfam; PF01542; HCV_core: I.
Pfam; PF01543; HCV_NS1: I.
Pfam; PF01560; HCV_NS2: I.
Pfam; PF01001; HCV_NS4: I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A38465; GNWVIC.
PDB; 1A10; 25-MAR-98.
PDB; 1JXP; 14-JAN-98.
PCB; 1NS3; G8-APR-98.
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MEROPS; U39.001;
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93.5%: Score 891: DB 1: i.e.
pred: No. 3.4e-77:
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                    MEDINE=91192160; PubMed-1849488;
Kato N., Hijikata M., Nakagawa M., Ootsuyama Y., Muraiso K.,
Ohkoshi S., Shimotohno K.;
Mohecular structure of the Japanese hepatitis C viral genome.";
FEBS Lett. 280:325-328(1991).
-!- FUNCTION: THE SHALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
-!- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral
precursor polyprotein, commonly with Asp or Glu in the P6
position, Cys or Thr in P1 and Ser or Ala in P1'.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91088550; PubMed-2175903; Kato N., Hijikata M., Ootsuyama Y., Nakagawa M., Ohkoshi S., Sugimura T., Shimotohno K., "Molecular Cloning of the numan hepatitis C virus genome from "Appanese patients with non-A, non-B hepatitis."; Proc. Natl. Acad. Sci. U.S.A. 87:9524-9528(1996).
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HCV_NS4b.
HCV_NS5a.
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HCV_NS1.
HCV_NS2.
HCV_NS3.
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IPR002518; H
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InterPro; IPR002522;
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HSSP; P26663; lJXP.
MEROPS; S29,001; -.
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MATRIX PROTEIN (POTENTIAL).
MAJOE ENVELOPE PROTEIN (POTENTIAL).
NONSTRUCTURAL PROTEIN NS! (POTENTIAL).
NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).
PROTEASE/HELICARE NS3 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS4 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
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LAPITAYSQQTRGLLGCIIISLTGRDKNQVDGEVQVLSTATQSFLATCVNGVCWTVYHGA
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SMART SMG0487; DEXDC: 1.
SMART SMG0487; DEXDC: 1.
SMART SMG0487; DEXDC: 1.
Core protein; Glycoprotein; Envelope protein; Helicase; ATP-binding;
Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
Iransmembrane; Nonstructural protein; Highrolase; Serine protesse.
INIT_MET 1 REMOVED: FROM CAPSID PROTEIN C BY THE CELLULAR AMINOPHPHIDASE.
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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                            InterPro; :PRC07095; RNA_pol_DS_PS.
InterPro; :PR067094; RNA_pol_PSvir.
Pfam: PF01543; HCV_capsid; l.
Pfam: PF01542; HCV_core; l.
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                                                                              Pfam: PF01539; HCV_CNV; 1.
Pfam: PF01560; HCV_NS: 1.
Pfam: PF01538; HCV_NS: 1.
Pfam: PF02090; HCV_NS3: 1.
Pfam: PF01006; HCV_NS3: 1.
Pfam: PF01006; HCV_NS4s: 1.
Pfam: PF01501: HCV_NS4s: 1.
Pfam: PF01501: HCV_NS4s: 1.
Pfam: PF01501: HCV_NS4s: 1.
Pf00091: HCV_NS4s: 1.
Pf00091: HCV_NS4s: 1.
Pf00001: P0186669: HCV_NS1: 1.
IPR002166; HCV_RdRP.
IPR001550; Helicase_
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87.9%;
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                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
6enome polyprotein (Contains: dapsid protein C (Core protein) (P22);
Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
(GP68) (GP0) (NS1); Protein E1 (GP32) (GP35); Envelope glycoprotein E2
(EC 3.4.22...); Proteins E1 (GP32) (Hepcolinin)
(EC 3.4.22...); Proteins Protein NS4A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)]

Repatitis C virus (isolate HC-JT) (HCV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tanaka T., Kato N., Nakagawa M., Cotsuyama Y., Cho M.C.,
Nakazawa I., Hijikata M., Ishimura Y., Shimotohno K.;
Nakazawa I., Hijikata M., Ishimura Y., Shimotohno K.;
Nacioular cloning of Lepatitis C virus genome from a single Japanese carrier: sequence variation within the same individual and among infected individuals...;
Virus Kes. 23:39-53(1992).

Virus Kes. 23:
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RNA_pol_DS_PS.
RNA_pol_PSvir.
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MEDLINE-92295714; PubMed-1318627;
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HCV_core.
HCV_env.
HCV_NSI.
HCV_NS3.
HCV_NS3.
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                                                                                                                                                            STANDARD;
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PDB; 1JXP; 14-JAN-98.
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InterPro; IPR002522;
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InterPro; IPR002519;
InterPro; IPR002531;
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InterPro; IPR004109;
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IPR007094;
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MEROPS; U39.001;
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MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELORE PROTEIN (POTENTIAL).
NONSTRUCTURAL PROTEIN NS1/R2 (POTENTIAL).
NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).
PROTEASE/HELICASE NS3 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
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Transmembrane; Nonstructural protein; Hydrolase; Serine protease;
3D-structure. ; REMOVED FROM CAPSID FROTEIN C BY THE
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                                Pfam: PF01539; BCV_env: 1.
Pfam: PF01550; BCV_Env: 1.
Pfam: PF01538; BCV_ENS: 1.
Pfam: PF02907; HCV_NS3: 1.
Pfam: PF01006; HCV_NS4a; 1.
Pfam: PF01001; HCV_NS4a; 1.
Pfam: PF01506; HCV_NS5a; 1.
Pfam: PF00571; helicase_C; 1.
Pfam: PF00998; Viral_RGRP; 1.
Probom: PP108062; HCV_NS1: 1.
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This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMH. outstation the European Bioinformatics institute of There are EMH. outstations on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                              Genome polyprotein [Contains: Capsid protein ( Core protein) (P22); Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7 Nonstructural protein NS2 (P21) (EC 3.4.22...); Protease/helicase NS3 (P70) (Hepacivizin) (EC 3.4.21.98); Nonstructural protein NS48 (P4); Nonstructural protein NS54 (P56); Nonstructural protein NS58 (P65); Nonstructural protein NS58 (P65); Nonstructural protein NS58 (P65); Norstructural protein NS58 (P65); CP70) (RNA-directed RNA polymerase) (EC 2.7.7.48)]. Hepatitis C virus (isolate HC-J8) (HCV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIROLOGY 188:331-341(1992).

-!-EUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

-!- CATALYIIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 postition, Cys or Thr in Pl and Ser or Ala in Pl'.

-!- CATALYIIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92230232; PubMed-1314459; Okada S.-I., Yamamoto K., Lizuka H., Tanaka T., Fukmoto H., Kurai K., Okada S.-I., Yamamoto K., Lizuka H., Tanaka T., Fukuda S., Tsuda F., Mishiro S.; "F.ll-length sequence of a hepatitis C virus genome having poor homology to reported isolates: comparative study of four distinct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLECCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLECCAPSID IS A COMPLEX OF PROTEIN C. AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29
                                                                                                                                    01-AGG-1992 (Rel. 23, Created)
01-AGG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007095; RNA_pol_bS_PS.
InterPro; IPR007094; RNA_pol_pSvir.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
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IPR002518; HCV_NS2.
IPR004109; HCV_NS3.
IPR000745; HCV_NS4.
IPR001490; HCV_NS4b.
IPR001490; HCV_NS58.
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InterPro: IPR00252; HCV_C
InterPro: IPR002521; HCV_C
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P26661;
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                                                                                                                                                   M POLYPOTOTELL, Transferase, RNA-directed RNA polymerase, W Transmembrane, Gaycoprotein, Iransferase, RNA-directed RNA polymerase, W Transmembrane, Nonstructural protein; Helicase: AIP-binding; Core protein; Coat protein; Helicase: AIP-binding; Transmembrane; Nonstructural protein; Helicase: AIP-binding; Transmembrane; Nonstructural REMOVED FROM CAPSID PROTEIN C BY THE CHAIN 116 191 MATRIX AMINOPEPTIDASE.

T. CHAIN 184 733 NONSTRUCTURAL PROTEIN NS. (POTENTIAL). MAJOR ENVELOPE FROTEIN NS. (POTENTIAL). TO CHAIN 1610 PROTEASE/HELICASE NS. (POTENTIAL). PROTEIN NS. (POTENTIAL). TO CHAIN 1620 MASTRUCTURAL PROTEIN NS. (POTENTIAL).
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Pfam; PF01539; HCV_env; I. Pfam; PF0156; HCV_NS1; I. Pfam; PF01538; HCV_NS2; I. Pfam; PF0207; HCV_NS3; I. Pfam; PF01006; HCV_NS4a; I. Pfam; PF01001; HCV_NS4a; I. Pfam; PF01506; HCV_NS5a; I. Pfam; PF00998; Viral_RdRP; I. ProDom; PP0186062; HCV_NS1; I. ProDom; PP0186062; HCV_NS1; I.
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FOLGEROWS STANDARD: PRT: 3033 AA.

FOLGEROWS STANDARD: PRT: 3033 AA.

TO "ANG"-599 (Rel. 23 I mats sequence update)

TO "ANG"-599 (Rel. 41. 1 mats sequence update)

TO "ANG"-
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NONSTRUCTURAL PRCTEIN NS4B (POIENTIAL).
RNA-DIRECTED RNA POLYMERASE (POIENTIAL).
                                                                                                                       Polyprotein; Gycoprotein; Transferase; RNA-directed RNA polymerase; Core protein; Coat protein: Envelope protein; Helicase; ATP-binding; Transmembrane; Nonstructural protein; Hydrolase; Serine protease. INIT_MET 1 REMOVED FROM CAPSID PROTEIN C BY THE
                                                                                                                                                                                   CELLULAR AMINOPEPTIDASE.
CAPSID PROTEIN ( POTENTIAL).
MAJOR ENVELOPE FROTEIN E (POTENTIAL).
MAJOR ENVELOPE FROTEIN E (POTENTIAL).
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CHARGE RELAY SYSTEM (BY
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CHARGE RELAY SYSTEM (BY
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69.8%; Pred. No. 5.3e-60;
tive 29; Mismatches 26
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Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4a; 1.
Pfam; PF01506; HCV_NS8a; 1.
Pfam; PF00271; Helicase_C: 1.
Pfam; PF00999; Viral_RGRP; 1.
ProDom; PD186062: HCV_NS1; 1.
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209 AA.

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VIQMYTNVDKDLVGWPAPQGSRSLIP-----CICGSSDL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----YLWTRHADVIPVRRRGDSRGSLLSPR--PIS-----YLKGSSGGPLLCPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 SAVATGACNNLIERAADVALKER----RPLVLVPREAPFSSIHLENMIKLSNLGAVILPA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AQQTRGLLGC:ITSLIGRDKNQVEGEVQ-IVSTAAQTFLATCINGVCWIVYHGAGTRTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 AQYGI,RLIDCLV-------GEEREVHFI,ISKAAQI,VMAT------ETLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 LPAKPQAMQAFLTEYCGAAASQIRVFGOND-----WMAPPASGSSAPNAMVICPCSTGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHOA TRAITH STANDARD: PRI; 321 AA.

99.5E1.7; 049.507;

16-0CT-2001 (Rel: 40, Last sequence update)

15-SEP-2003 (Rel: 42, Last annotation update)

15-SEP-2003 (Rel: 42, Last annotation update)

Protease HhoA, chloroplast precursor (EC 3.4.21.-).

PHOA OR A FA1618370 OR F28312.30.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAOJ:

MEDLINE-20437337; PubMed=10984043;

MEDLINE-20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.J., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAOJ, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piam: PF02441; Flavoprotein; 1.
Hypothetical protein; Lyase; Decarboxylase; Complete proteome.
SEQUENCE 209 AA; 22367 MW; GIFD081CC495D3F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - I - SIMILARITY: BELONGS TO THE POLYPRENYL P-HYDROXYBENZOATE PHENYLACRYLIC ACID DECARBOXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.1%; Score 87; DB 1; Length 209; 6.2%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61: Indels
16-0CT-2001 (Rel. 40, Created)
Locar-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Probable aromatic acid docarboxylase (EC 4.1...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --APGFYHQ----PQSVEDLVDFVVARILNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; H83144; H83144.
InterPro; IPRC03382; Flavoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004818; AAG07406.1; -.
                                                                                                                                                                                                                                                Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 SPKGP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                opportunistic pathogen.
                                                                                                                                                                              Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Lensch M.H.A., Sokolenko A., Herrmann R.G.;
"Identification and characterization of the chloroplast HhoA protease,
a homolog to the bacterial periplasmic protease HhoA.";
Submitted (DEC-1998) to the BMBL/GenBark/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                             CAUTION: Ref.2 sequences differ from that shown due to erroneous gene model prediction. AT4G18379 and AT4G18375 were originally
                                                                                                                                                                                                                                                                                                                                                                                                   "The chloroplast lumen from Arabidopsis thaliana.";
Submitted (JUL-2001) to the SWISS-PROT data bank.
-!- SUBCELLULAR LOCATION: Chloroplast: within the thylakoid lumen.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 72-82; 96-110; 150-159; 178-211 AND 306-320
                                                                                                                                                                                                                                                                                                                                                                                      Schubert M., Peterson U., Funk C., Baas B., Schroeder
Kieselbach T.;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                   MEDLINE-20083488; PubMed-10617198;
                                                                                                                                                                                                                                                                                                                                                                     Nature 402:769-777(1999).
                                                              SIRAIN-cv. Columbia;
                  SEQUENCE FROM N.A.
                                                  [2]
SEQUENCE FROM N.A
    NCBI_TaxID-3702;
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between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no re-

There are no restrictions on its

EMBL outstation

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3.1;
        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcc/
                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SLLSPRPISYLK------GSSGGPLLCPA 148
                                                                                                                                                                                                                                                                                                                                                            117 LTDEENGKIEGTG------SGFVWDKLGHIVTNYHVIAKLATDQFGLQRCK 161
                                                                                                                                                                                                                                                                                                                                                                                     59 ----GAGIRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRSLIPCTCGSSDLYLVTRHAD 113
                                                                                                                                                                                                                                                                                                                                                                                                  218 AI-----GNPYGYENTLIIGVVSGLGREIPSPNGKSISEAIQTDADINSGNSGGPLLDSY 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ou ui si
                                                                                                                                                                                                                                                                                                              Saps
                                                                                                                                                     Chloroplast; Thylakoid; Transit peptide. CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enkaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                              CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                       (POTENTIAL)
institutions as long as its content
                                                                                                                                                                                                                                                                                      DB 1; Length 321;
                                                                                                                                                                                                                                                                                                                                     22 LIGRDKNQVEGEVQIVSTAAQIFTATCINGVCW-----TVYH----
                                                                                                                                                                                                                                                                                                              60; Indels
                                                                                                                                                                                                                                                   R -> G (IN REF. 1).
68DB81E0BD27A7A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 GHAVGIFRAAVCIR---GVAKAVDF-IPVESLETIM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
26-FFB-2003 (Rel. 41, Last annotation update)
Angio-associated migratory cell protein.
                                                                                                                                                                                                                                                                                                 Pred. No. 0.88;
                                                                                                                                                                            THYLAKOID.
PROTEASE HHOA.
                                                                                                                                                                                                                                                                                                              26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       8.8%; Score 84;
                                                                                                                  InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                    POLY-GLU
                                                     EMBL; AF114386; AAF24060.1; -.
EMBL; AL021710; CAA16717.1; ALT_SEQ.
EMBL; AL161548; CAB78839.1; ALT_SEQ.
MEROPS: S01.279; -.
interpro; IPR001940; Proteasc2C.
                                                                                                                                                                                                                                                              34691 MW;
                                                                                                                             Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
                                                                                                                                                     Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                 22.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                  114 VIPVRRRGDSRG-----
                                                                                                                                                                                                                                                                                                              48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                      321
145
145
186
264
40
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                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                              321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
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Q13685;
                                                                                                                                                                                                              ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                          TRANSIT
                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                   DOMA: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
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spirochete.";
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SEQUENCE
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DOMAIN
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DEG:_ARATH
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      80 THE PRESENTANT WAS A WAY OF THE PRESENTANT OF
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                           between the Swiss Institute of Bicinformatics and the EMBL outstation. The Buropean Boinformatics institute. There are no restrictions on its use by non-profit institutions of a sits content is in no way modified and this statement is not removed. Usage by and for confinencial entities requires a license agreement (See hitp://www.isb.sib.ch/announce/or send an email to license@isb.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 WTVYHGAGTRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRSL----TPCTGGSSDLYLV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 TRHADVIPVRRA---GDSRGS-----LLSPRPISYLKGSSG--GPLLCPA-----148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 -----VIPDGKRAVVGYEDGTIRIWDIKQGSPIHVLKGTHGHQGGPITCVAANQDGSLILT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 WMEWHI------PRAPVLLAGT-ADGNTWMWKVPNGDCKTFQGPNCPATCGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser C.M., Norris S.J., Meinstock G.M., White C., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Ciayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M. Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              freconema pallidum.
Bacteria: Spirochaetes: Spirochaetales: Spirochaetaceae; Treponoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GHAVGIFR----AAVCIRGVAKAVDFIPVESD, 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 GSVDCQAKLVSATICKVVGVFRPETVASQPSLGEGEESESNSVEST 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.6%; Score 82; DB 1; Length 452; 25.3%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEPARIN-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DA1413D25EB236C0 CRC54;
                                                                                                                                                                                                                                                                                                                        MIM. 603488; ...
GO; GO:0008201; F:heparin binding activity; TAS.
GO; GO:0008202; F:heparin binding activity; TAS.
GO:0008202; WD40; 8.
EMART; SM00320; WD40; 8.
PROSITE: PS00320; WD_REPEATS_1; 1.
PROSITE: PS00829; WD_REPEATS_2; 6.
RPOSITE: PS50294; WD_REPEATS_REGION; 1.
REPEATS WD LEPARIN-BINDING (POTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ti36_TREPA STANDARD; PRT; 485 AA. 083172; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation ipdate) Hypothetical lipoprotein TPC136 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLU.
WD 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WD 2. WD 2. WD 4. WD 5. WD 6. WD 8. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Nichols;
MEDLINE-98332770; Pubmed-9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49015 MM;
                                                                                                                                                                                                                                    EMBL; M95627; AAA68889.1; -. PIR; I39383; I39383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 25.3
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
77
138
180
220
220
261
363
                                                                                                                                                                                                                                                                                               Genew; HGNC:18; AAMP.
MIM; 603488; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the FWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commorcial entities regulres a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 TDSDK-----KVMSIAIDGNTFVIACVPGIGVYKHCVNGAGSSSIGITASPSTETCSQHA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 NVDKDLVG-----WPAPQGSRSLIPCTC----GSSDLYLVTRHADVIP-----VR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GSSGGPLLCPAGHA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 T----LVGGTSKPFWLVPGGTGNNGNCGCGGGGGSSSSSSCIHIWLVPGGTGNNGNCG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 TGRDKNQVEGEVQIVSTAAQTFLATCI--NGVCWTVYHGAG---TRTIASPKGPVIQMYT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                 -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98175982; PubMed-9507020;
Itahaki H., Naveh L., Lindahl M., Cook M., Adam Z.;
'Identification and characterization of Degp, a serine protease
associated with the luminal side of the thylakoid membrane.";
J. Biol. Chem. 273:7094-7098(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL LIPOPROTEIN TP0136.
N-ACYL DIGLYCERIDE (POTENTIAL).
GLY/SER-RICH.
GLY/SER-RICH.
GLY/SER-RICH.
POLY-SER.
                                                                                                  -!- SIMILARITY: BELONGS TO THE TP013X FAMILY OF LIPOPROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.6%; Score 82; DB 1; Length 485; 24.2%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEGI_ARATH STANDARD; PRT; 437 AA. 022603, O9EKBS; 16-OCT-2001 (Re1. 4C, Last Sequence update) 16-OCT-2001 (Rel. 4C, Last Sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Proclease Do-1ike 1, chloroplast precursor (EC 3.4.21.-). DEGP1 OR DEGP OR ATSG7925 OR K16Ni2.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C7A4CEEDC7DC5CED CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: AE001199; AAC65137.1; ALT_INIT.
TIGR: TP0136; -.
Hypothetical protein: Lipoprotein: Membrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 RRGDSRGSLLSPRPISYLK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48984 MW;
Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444
485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 VG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GG 258
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210 PK--NKLRPIPVGVSADLLVGQKVFAIGNPFGLDHTLTTGVISGLRREIS--SAATGRPI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Autolysis of proproteinase E in bovine procarboxypeptidase A ternary complex gives rise to subunit 111."; FEBS Lett. 277:37-41(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pignol D., Gaboriaud C., Michon I., Kerfelec B., Chapus C.,
Pignol D., Gaboriaud C., Michon I., Kerfelec B., Chapus C.,
Fontecilia-Camps J.C.,
Fontecilia-Camps 
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proproteinase E precursor (Procarboxypeptidase A complex component III) (Procarboxypeptidase A-S6 subunit III) (PROCPA-S6 III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eskaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostemi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                               134 SYL------KGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDF-IPVESL 176
                                                                                                    Venot N., Sciary M., Puigerver A., Desnuelle P., Laurent G., "Amino acid sequence and disulfide bridges of subunit III, a detective cardopotiates present in the bovine pancreatic 6 Sprocarboxypeptidase A complex ", Eur. J. Biochem. 157:91-99(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pascual R., Vendrell J., Aviles F.X., Bonicel J., Wicker C., Puigsorver A.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pancreas, Digestion, 3D-structure.
ACTIVATION PEPTIDE.
PROPROTEINASE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                    01-NOV-1988 (Rel. 09, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                           253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 14-253, AND DISULFIDE BONDS.
MEDLINE-86220198; PubMed-3519215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-25.
MEDLINE=91099520; PubMed-2269366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00020; Tryp_SPc; 1.
PROSITE: PSS50240; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS: 1.
PROSITE: PS00135; TRYPSIN_ESR: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease homolog;
PRJPEP 1
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253
57
103
206
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227
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PDB; IPYT; 27-JAN-97.
MEROPS; S01.983; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ros taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                        CAC3_BOVIN
PC5805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
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                                                                                                                                                                                                                                                          CAC3_BOVIN
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                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the PMIS, ottstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its centent is in a way modified and this statement is not removed. Usage by and for commercial entities requires a bronned afterned (See http://www.ish-sib.ch/announce/or send an email to licensetisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 VYHGAGTRIIASPKGPVIQMY-------PA
                                                                                                                                                                                                                                                   STRAIN-CV. Columbia;
Kieselbach T., Bystodi M., Schroeder W.P.;
Submitted (JüL-2000) to the SWISS-PRCT data bank.
-!- FUNCTION: SERINE PROTEASE THAT IS REQUIRED AT HIGH TEMPERATURE.
MAY BE INVOLVED IN THE DEGRADATION OF DAMAGED PROTEINS. IN VIVO.
CAN DEGRADE BETA-CASEIN.
-!- ENZYME REGULATION: INHIHITED BY PHENYLMETHYLSGLEONY; FLGORIDE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transit peptide; Chloroplast; Ihylakeid. CHLOROPLAST (POIENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
HSPPSSQLSNST -> SSTLMILISPESSHL (IN REF.
                              Kaneko I., Katoh I., Sato S., Nakamura A., Asamizu E., Tabata S.; "Structural analysis of Arabidopsis thallara chromosome 3. II. Sequence features of the 4.251,695 by regions covered by 90 Pl. TAC and Bac closes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: BOUND TO DUMINAL SIDE OF THE THYLAKOLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
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(V > 1 (IN REF. 2).
(V > 5 (IN REF. 2).
(G > 8 (IN REF. 2).
(G > 0 (IN REF. 2).
(L > 0 (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- INDUCTION: By heat shock.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY $20.
-i- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEASE DO-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERINE PROTEASE.
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InterPro; IPR001946; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THYLAKOID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF028842, AAC39436.1: -.
EMBL, APC0C371; BAB02539.1: -.
EMBL, APO01302, BAB02539.1: JOINED.
MEDLINE~20363099; PubMed-10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART: SM00228; PDZ; 1.
PROSITE; PS50:06; PDZ; 1.
Hydrolase; Serine protease;
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
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                                                                                                                                                         DNA Res. 7:217-221(2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O-PHENANTHROLINE
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324
324
271
201
12
                                                                                                                           BAC clones.
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ACT_SITE
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2cca pellucida sperm-binding protein 3 precurso: (2cna pellucida
diycoprotein 2P3) (Sperm receptor) (2cna pellucida protein C)
(Fragment).
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PIR; S70401; S70401.
InterPro; IPR001507; Endoq:in/CD105.
Pfam; PR00100; zona_pollucida; 1.
SMART; SM00241; ZP; 1.
PROSITE: PS00682; ZP_DOMIN; 1.
                                                                                                                                                                    IISSUE-Ovary;
MEDLINE=95143578; PubMed=7841460;
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Live 23; Mismatches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BMB outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 --PMNQNHAARSSLRSRRHVTEEADVTVGPLIFLGKAGDPAG------TEGLASA 374
                                                                                                                                                                                                                                                                                                                                                             "Cioning and characterization of zona pellucida genes and cDNAs from a variety of mammalian species: the ZPA, ZPB and ZPC gene families."; DNA Seq. 4:361-393(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53; Indels 15; Gaps
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ZONA PELLUCIDA SPERM-BINDING PROTEIN 3.
EXIRACELLULAR (POTENTIAL).
Oryctolagus cuniculus (Rabbit).
Eukarycta; Metazoa: Chordata; Craniata; Verlebrata; Euteleoslomi;
Mammalia; Eutheria: Lagomorpha: Leporidac; Oryctolagus.
                                                                                                                                                                                                                                                                                           Harris J.D., Hibler D.W., Fontenot G.K., Hsu K.T., Yurewicz E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal; Sulfation; Sporm; Receptor; Transmombrane; Extracollular matrix; Multigene family.

NON_TER 1 1 1 POTENTIAL.
CHAIN 19 415 7000 1000 1000 415
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26.7%; Pred. No. 9.5;
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Job time : 26 secs
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(Rel. 33, Created) (Rel. 33, Last sequence update) (Rel. 33, Last annotation update)

01-FEB-1996 (01-FEB-1996 (01-FE ZP3\_RABIT P48833;

RESULT 15 2P3\_RABIT ID 2P3\_R AC P4883 DT 01-FE DT 01-FE

415 AA

PRT;

STANDARD:

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 27, 2003, 11:44:04; Scarch time 42 Seconds (without alignments) 416.7% Million cell updates/sec Run on:

US-09-965-594-1 953 | MAPITAYAQQTRGLLSGIIT......GVAKAVDFIPVESLETIMRS 182 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 9 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 99% Listing first 45 summaries

Database :

PIR\_76:\* 1: pir1:\* 2: pir2:\* 3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SCALANDAMOS	DB ID Description	genome					J genome	A45573	\$18030	JC5620	GNWVJ8	JQ1303	T08841	T08839	H83144	139383	B71360	T48399 heat shock tr		T18234	H89566	B71284	A84212		H81775	CPEOA3	S70401	S23441 hypothetical pr	C81200	
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Result	No.	, 4	7	٣	*7	S	9	7	ω	5	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	

hypothetical prote	hypothetical prote	protein F22G5.28 [	hypothetical prote	hypothetical prote	C4-dicarboxylate t	phosphate ABC tran	hypothetical prote	transferrin-bindin	transferrin-bindin	latent transformin	serine proteinase	hypothetical prote	htrA-like serine p	chitinase (EC 3.2.	granzyme M (EC 3.4
C72705	A75335	G86208	F90978	S76033	H82044	H84203	T04533	C81832	F81196	A55494	A89967	T49806	н97199	S65752	A55634
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74 7.8	74 7.8	74 7.8			73.5 7.7						7.7 7.7	7.7 7.7	7.7 7.7	7.7 7.7	72.5 7.6

## ALIGNMENTS

RESULT 1 GMWVC3 GENOME DOLVDFOLEID - hepatitis C virus (strain ECV-1)	
N.Communication of the control of th	S.
C.Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 19-Jan-2001 C.Accession: A39166: P06403; P00404	
Richoo, Q.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, C	ن
A.Title: Genetic organization and diversity of the hepatitis C virus. A.Pofornoo compon, 320146, MITTLE 0112056, DMID: 042704	
A.Accession: A39166	
A; Molecule type: mRNA A; Residues: 1-3011 <cho></cho>	
A;Cross-references: GB:M62321; NID:g329873; PIDN:AAA45676.1; PID:g329874 B.Charler G. G. McCmish B. + Holmes F. C Dow B Deritherer T. F Follett. F Var	Š
J. Gen. Virol. 73, 1131-1141, 1992	5
A;Title: Analysis of a new hepatitis C virus type and its phylogenetic relationshi A:Reference number: P00393; MUID:92268871; PMID:1316939	<u> </u>
A; Accession: P00403	
A.Molecule type: genomic RNA A.Wesidies: 1577-1673 (CHA)	
A:Cross-references: DDBJ:D10128	
A; Experimental source: isolates E-bi6	
A. A. Cression: 1900 4 0 4 A. Cression: 1900 4 0 A. Cression	
A: Molecule type: qenomic RNA	
A;Residues: 1577-1633 <ch2></ch2>	
A: Experimental Source: Isolates E: D17	
; superiaminty: neparints cyntus geneme potetoutaminty: neparints cyntus geneme protein; dygoprotein; hydrolase; nonstr C: Kewyords: ATP; capsid protein; envelope protein; dygoprotein; hydrolase;	I.
F:1-115/Product: capsid protein C *Status predicted <cpc></cpc>	
F:116-191/Product: envelope protein M *status predicted <epm></epm>	
F. 390-729/Product: major envelope process. Practus predicted Americal 290-729/Product: monstructural process status predicted ANSI	
F;730-1006/Product: nonstructural protein NS2 #status predicted <ns2></ns2>	
F:1007-1615/Product: hepacivirin #status predicted <ns3></ns3>	
F:1230-1237/Region: nucleotide-binding mouth A (F 100p)	
F:1316-1319/Region: DEXH motif	
F:1516-1862/Product: nonstructural protein NS4a #status predicted <n4a> F:1863-2013/Droduct: nonstructural protein NS4h #status predicted <n4a></n4a></n4a>	
F;2014-3011/Product: nonstructural protein NSS #status predicted <nss></nss>	
F:196, 209, 234, 305, 325, 417, 423, 430, 448, 476, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 2	5
Best Local Similarity 98.4%; Pred. No. 5.7e-81; Matches 179; Conservative 3; Mismatches 0; Indels 0; Gaps 0;	
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A; Note: neither amino acid nor nucleotide sequence is given A; Note: neither amino acid nor nucleotide sequence is given C; Superfamily: hepatitis C virus genome polyprotein C; Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase; nonstruc C; Keywords: ATP; capsid protein; envelope protein G status predicted <CRC> F.116-191/Product: envelope protein M status predicted <ERP> F; 192-389/Product: major envelope protein NSI *status predicted <NSI> F; 730-1006/Product: nonstructural protein NSI *status predicted <NSI> F; 1007-1615/Product: nonstructural protein NSI *status predicted <NSI> F; 1230-1237/Region: nucleotide-binding motif A (P-loop) F; 1316-1319/Region: nucleotide-binding motif B F; 1316-1319/Region: DEXH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Accession: A16814
A:Molecule type: genomic RNA
A:Rosidues: 1.301; LNC>
A:Cross-references: GB:A67463; NID:g329737; PIDN:AAA45534.1; PID:g329738
A:Cross-references: GB:A67463; NID:g329737; PIDN:AAA45534.1; PID:g329738
B:Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
A:Title: Genomic structure of the human prototype strain H of hepatitis C virus: com A:Reference number: A41546; MUID:g2052286; PMID:165880C
                                                                                                                                                                                                                          NyContains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (noust: protein NS4a; nonstructural protein NS4b; nonstructural protein NS5 C; Species: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                 A;Note: host Homo sapiens (man)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-Jan-2001
C:Accession: A36814; A41546
C:Accession: A36814; A41546
C:Accession: A36814; A41546
C:Batterior G: Batterior (Batterior A)
C:Batterior (Batterior Cenemic structure of the human prototype strain H of hepatitis C
                                                                                                                                                                                        genome polyprotein - hepatitis C virus (strain H) N;Contains: capsid protein C; envelope protein M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A: Reference number: A36814
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A: Title: The S'-terminal sequence of the hepatitis C virus genome.
A: Article: The S'-terminal sequence of the hepatitis C virus genome.
A: Article: The S'-terminal sequence of the hepatitis C virus genome.
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A: Residues: 1:53 COK2>
A: Cossereferences: GB: DOBB31: NID: 9221511; PIDN: BAA00765.1; PID: 9221512
A: Experimental source: isolate HC-JI
C: Superfamily: hepatitis C virus genome polyprotein
C: Superfamily: hepatitis Diotein NS2 *stalus predicted <NS2>
F: 1007-1015/Product: nonstructural protein NS4 *stalus predicted <NAA>
F: 1863-2013/Product: nonstructural protein NS5 *stalus predicted <NAA>
F: 1863-2013/Product: nonstructural protein NS5 *stalus predicted <NS2>
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Fil616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
Fil6863-2013-Product: nonstructural protein NS4 #status predicted <N4B>
Fil2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
Fil96,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,224
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N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4
protein NS43; nonstructural protein NS4b; nonstructural protein NS5
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change
C;Accession: A40244
R;Chen, P.J.; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen,
Virology 188, 102-113, 1992
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                                                                                                                                97.3%; Score 927; DH 1; Lo
96.2%; Pred. No. 1.9e-79;
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A.; Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onish, E.; J.; Virol. 65, 1105-1113, 1991
A.; Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onish, E.; A.; Moricular and organization of the hepatitis C virus genome isclated from human A.; Reciprocular and organization of the hepatitis C virus genome polyprotein:
C.; Superfamily: hepatitis C virus genome polyprotein:
C.; Superfamily: hepatitis C virus genome polyprotein:
C; Superfamily: hepatitis C virus genome isciated from human
C; Superfamily: hepatitis C virus genome isciated from
A;Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the A;Reference number: A40244; MUID:92236206; PMID:1314449
A;Accession: A40244
A;Accession: A60244
A;Accession: A60244
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N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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90.1%; Pred. No. 4.16-76;
ive 12; Mismatches 6;
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C. Species: hepatitis C virus

C. Species: hepatitis C virus

C. Date: 30-Jun-1922 *Recuence_revision 30-Jun-1992 *Lext_change 19-Jan-2001

C. Species: hepatitis C virus

C. Date: 30-Jun-1922 *Recuence_revision 30-Jun-1992 *Lext_change 19-Jan-2001

C. Date: 30-Jun-1932 *Recuence_revision 30-Jun-1992 *Lext_change 19-Jan-2001

R. Kato, N.: Hijikata, M.: Ootsuyama, Y.: Nakagawa, M.: Ohkoshi, S.: Sugimura, T.: &

R. Kato, N.: Molecular cloning of the human hepatitis C virus genome from Japanese pat:

A. Reference number: A39253; MUID: 91088550; PMID: 2175903

A. Residues: 13010 *KAY.>

A. Residues: 13010 *KAY.>

A. Residues: 13010 *KAY.>

A. Residues: 13010 *KAY.>

A. Title: Japanese isopates of the non-b hepatitis viral genome show sequence in the companies of the non-b hepatitis viral genome show sequence in the companies isolates of the non-b hepatitis viral genome polyprotein have not been determined.

A. Molecule type: genomic RNA

A. Residues: 2560-7707 *KASA

A. Residues: 2560-770 *KASA

A. Re
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F;1863-2013/Product: nonstructural protein NS4b #status predicted <NAB>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,325,417,423,430,448,532,556,576,623,645,1213,1255,2041,2077,
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                                                                                                                                                                                                                                                                                                                                                                            GIRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRSLIPCTCGSSDLYLVIRHADVIPVRRR 120
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N;Contains: capsid protein C; envelope protein M; major envelope protein E;
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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                                                                                                                                                                                           1 MAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGA
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Length 3010;
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93.5%; Score 891; DB 1;
89.0%; Pred. No. 5.1e-76;
Live 15; Mismatches 5;
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A:Variety: isolate JKI
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 23-Mar-2001
C:Accession: 518030, 533570; A48332; S18029
R:Bionda, M.; Kaneko, S.; Masshi, U.; Kobaysshi, K.; Murakami, S.
R:Bubmitted to the EMBL Data Library, September 1991
A;Description: A whole genome of hepatitis C virus cDNA was isolated from a single p
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A.Residues: 1-3010 c40NN
A.Residues: 1-3010 c40NN
A.Residues: 1-3010 c40NN
A.Cross-references: EMBL.X61596; NTD:959478; PIDN:CAA43793.1; PID:959479
A.Experimental source: isolate JK1 from an individual
B.Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 128, 163-169, 1993
A.Title: Sequence analysis of putative structural regions of hepatitis C.
A.Reference number: A48332; MUID:93119270; PMID:8380322
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A;Accession: $18030
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A Accession: A45573
A Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Experimental source: HCV-JT
A, Cross-references: GB:D11168: GB:D01171; NID:q221612; PIDN:BAA01943.1; PID:q221613
A, Cross-references: GB:D11168: GB:D01171; NID:q221612; PIDN:BAA01943.1; PID:q221613
A, Cross-references: GB:D11168: GB:D01171; NID:q221612; PIDN:BAA01943.1; PID:q221613
A, NOTE: sequence extracted from NBI backbose (NGBIP:10626, NGBIP:106204)
C, Superfamily: hepatitis C virus genome polyprotein
C, Superfamily: hepatitis C virus genome polyprotein
C, Superfamily: hepatitis C virus genome polyprotein
F; 2.115/Product: capsid protein M *status predicted <PPM>F:16-191/Product: capsid protein NSI *status predicted <NS2>
F; 192-189/Product: nonstructural protein NSI *status predicted <NS2>
F; 1007-1615/Product: nonstructural protein NSI *status predicted <NAA>
F; 1312-1317/Region: nucleotide-binding motif A (P-100P)
F; 1316-13862/Product: nonstructural protein NSI *status predicted <NAA>
F; 18616-1862/Product: nonstructural protein NSI *status predicted <NAA>
F; 18616-1862/Product: nonstructural protein NSI *status predicted <NAA>
F; 1861-18010/Product: nonstructural Protein NSI *status predicted <NAA>
F; 186
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NCOntains: capsid protein: C evelope protein M: hepacivitin (SC 3.4.21.38) (nonstructu protein NS4s; nonstructural protein NS5s; least protein NS5s; least
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N;Contains: capsid protein C: envelope protein M: hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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183,34 (1113 (1111) (1111) (111) (111) (111) (111) (111) (111) (111) GSKTLAGPKGPTTGMYTNVDQOLVGWPAPPGARSMYPCTGGSSDLYLVTRHADVVPVRRR 1145
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                                                                                                                                                                                          GDSRGSIJJSPRPISYLKGSSGGPLJJCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETIK 180
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88.5%; Pred. No. 2.3e-75;
Live 15; Mismatches 6; Tidels
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hes 161; Conserv
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A; Motecule type: genomic RNA
A; Residues: 1.547, T',549-621, V',623-624,'S',626-652,'DL',655-751,'T',763-782 < HDW;
A; Residues: 1.547, T',549-621,'V',623-624,'S',626-652,'DL',555-751,'T',763-782 < HDW;
A; Cross references: EmBL:x61591
A; Note: this sequence is inconsistent with the nucleotide translation
A; Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue
as Trp, and TTC for residue 71 as Ser
A; Note: sequence extracted trom NOBI backbone (NOBIN:121747, NOBIP:121748)
C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis
C; Superfamily: hepatitis mevelope protein NS1 *status predicted < NS2>
F; 192-389/Product: nonstructural protein NS1 *status predicted < NS2>
F; 1307-1006/Product: nonstructural protein NS2 *status predicted < NS2>
F; 1312-1317/Region: nucleotide-binding motif A (P-loop)
F; 1312-1317/Region: DEXH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F:1616-1862/Product: nonstructural protein NS4a *status predicted <N4A>
F:1868-2013/Product: nonstructural protein NS4b *status predicted <N4B>
F:2014-3010/Product: nonstructural protein NS5 *status predicted <NS5>
F:2014-3010/Product: nonstructural protein NS5 *status predicted <NS5>
F:196,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate
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N:Contains: capsid protein C; envelope protein M: hepacivirin (EC 3.4.21.98) (nonstraprotein Ns42, nonstructural protein Ns4b; nonstructural protein NS5
C:Species: hepatitis C virus
C:Species: hepatitis C virus
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
C:Accession: JC5620
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A;Title: The complete coding sequence of hepatitis C virus genotype 5a, the predomin. A;Reference number: JCS620; MUID:97366593; PMID:9223423
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86.8%; Pred. No. 1.9e-73;
ive 15; Mismatches 9; Indels
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C; Species: hepatitis C virus

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A.Crossludes: 2076.27 Natl.

A.Crossludes: 2076.27 Natl.

C. Superfamily: hepatitis C virus genome polyprotein
C. Superfamily: hepatitis C virus genome polyprotein
C. Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase; nonstruct capsid protein C *status predicted <CPC>
F.1-115/Product: capsid protein C *status predicted <CPC>
F.1-115/Product: envelope protein B *status predicted <NEN>
F.192-389/Product: major envelope protein B *status predicted <NSI>
F.190-733/Product: monstructural protein NSI *status predicted <NSI>
F.134-1216/Product: nonstructural protein NSI *status predicted <NSI>
F.101-1619/Product: nonstructural protein NSI *status predicted <NSI>
F.101-1619/Product: nonstructural protein NSI *status predicted <NSI>
F.134-122/Region: nucleotide-binding motif B (P-loop)
F.1350-1323/Region: DEXH motif
F.1550-1866/Product: nonstructural protein NSI *status predicted <NAB>
F.1367-2017/Product: nonstructural protein NSI *status predicted <NAB>
F.1367-2017/Product: nonstructural protein NSS *status predicted <NAB>
F.1367-2017/Product: nonstructural protein NSS *status predicted <NAB>
F.1265,205,233,299,305,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,20
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N.Contains: capsid protein C: envelope protein M: hepacivirin (EC 3.4.21.98) (nons
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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F;1867-2011/Product: nomstructural protein NS4b #status predicted <N4B>
F;2018-3033/Product: nomstructural protein NS5 #status predicted <NOS>
F:196,209,234,305,325,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GDSRGSLLSPRPISYLKGSSGGPLLCPAGHAVG:FRAAVCTRGVAKAVDFIPVESLETIM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.9%; Score 714; DB 1; 70.9%; Pred. No. 3.5e-59; tive 26; Mismatches 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity 70.9°
129; Conservative
A; Accession: PQ0559
A; Molecule type: mRNA
A; Residues: 2678-2729 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1210 RT 121:
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Best Local 9
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A. Molecule type: genomic RNA
A. Cross references: GB: 0.0988: GB: D01221: NID: q221608; PIDN: BAA01761.1; PID: q221609
A. Molecule type: genomic RNA
A. Cross references: GB: 0.0988: GB: D01221: NID: q221608; PIDN: BAA01761.1; PID: q221609
A. Cross references: GB: 0.0988: GB: D01221: NID: q221608; PIDN: BAA01761.1; PID: q221609
A. Cross references: GB: 0.0988: GB: D01221: NID: q2268871: PMID: 131693
A. Molecule type: qenomic RNA
A. Reference number: PQ0393: NUID: q2268871: PMID: 1316939
A. Molecule type: qenomic RNA
A. Residues: 2578-2754
A. Molecule type: qenomic RNA
A. Residues: Commun : 181, 279-285, 1951
A. Makazawa, T.: Molto, S.: Hijikata, M.; Shimotchuc
Blochem: Biophys. Res: Commun : 181, 279-285, 1951
A. Title: Distribution of plutal HCV types in Japan.
A. Reference number: PQ0554: MUID: q2068204; PMID: 1720369
                                                                       A. Cross-references: 4.044 Note: total definition of the nucleotide sequence in South Africa A. Experimental source: genotype 5a, which predominates in South Africa A. Experimental source: genotype 5a, which predominates in South Africa A. Note: the translation of the nucleotide sequence is not complete in this paper C. Superfamily: hepatiliz C virus genome polyprotein
C. Superfamily: hepatiliz C virus genome polyprotein
C. Seywords: ATP: 91ycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; E. 2-115, Product: capsid protein C *status predicted <PE>F. 2-15, Product: envelope protein C *status predicted <PE>F. 384-408/Region: hypervariable *status predicted <PE>F. 384-408/Region: hypervariable *status predicted <PE>F. 390-730/Product: nonstructural protein NSI *status predicted <PE>F. 31-1007/Product: nonstructural protein NSI *status predicted <PE>F. 31-318/Region: nucleotide-binding mobile A (NSI)
F. 31317-1328/Region: nucleotide-binding mobile B (F. 31317-1320/Region: DEXH motif
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Ncontains: capsid protein C; covolope protein M: hepativitin (EC 3.4.21.98) (nonstructu NS4s) nonstructural protein NS5
C; Species: hepatitis C virus
C; Species: hepatitis C virus
C; Species: a.P-oec-1992 *sequence_revision 31-Dcc-1992 *text_change 19-Jan-2001
C; Accession: A40250; pc0397; pc0559
R; Okamoto, ii.; Kurai, K.: Okada, S.I.; Yamamoto, K.: Lizuka, H.: Tanaka, T.: Fukuda, S.; Virology 188, 33. 341, 1992
A; Title: Full-length sequence of a hepatitis C virus genome having poor formology to repatitie: Full-length sequence of a hepatitis C virus genome having poor formology to repatitie: commence of a hepatitis C virus genome having poor formology to repatities commence.
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+ 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTELATCINGVCWTVYHGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fil617-1863/Product: nonstructural protein NS4a #status predicted <N4A> F;1864-2014/Product: nonstructural protein NS4b #status predicted <N4B> F;2015-3014/Product: nonstructural protein NS5 #status predicted <NS5> F;2210-2249/Region: interferon sensitivity determining #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                          A; Molecule type: mRNA
A; Residues: 1-3014 <CHA>
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| RS 1208
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A;Gene: PA4019
C;Superfamily: dedF protein
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Best Local Similarity
Matches 55; Conserv
      Residues: 1-2976 < ERK >
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A;Status: preliminary
A;Molecule type: DNA
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H83144
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                                                                                                                                                                                                                                                                                                                                                                                                                                           polyprotein - dourousoull hepatitis GB virus A
C.Species: dourousoull hepatitis GB virus A
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C.Accession: 108841
B.Erker, J.C.: Desai, S.M.: Leary, T.P.: Chalmers, M.L.: Montes, C.C.: Mushahwar, I.K.
J. Gen, Virol. 79, 41-45, 1998
A.Title: Genomic analysis of two GB virus A variants isolated from captive monkcys.
A.Reference number: 216486; MUID:98120818; PMID:9460920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
T088139
T098139
T098139
C;Species: marmoset hepatitis GB virus A
C;Species: marmoset hepatitis GB virus A
C;Species: marmoset hepatitis GB virus A
C;Species: 13-Jul-1999 *sequence_revision 23-Jul-1999 *tcxt_charge 17-Nov-2600
C;Accession: T08839
B;Erker, C.C.; Desai, S.M.; Leary, T.P.; Chalmers, M.L.; Montes, C.C.: Mushahwar, 1.K.
J, Gen. Virol. 79, 41-45, 1998
A;Title: Genomic analysis of two GB virus A variants isolated from captive monkeys.
A;Reference number: 216486: MCID:95120818; PMID:9460926
A;Status; translated from GB/EMBL/D0BJ
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C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 TRTIASPKGPVIQMYTNVDKDINGWPAPOGSHSIJPGTGGSSDLYLVJRHADVIPVRRHG 121
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                                                                                                                                                                                                                                          GDSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCIRGVAKAVDFIPVESLETIM 180
                                                                                                                                                                61 GTRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRSLTFGTCGSSSLYLVTRHADV7FVRR 120
                                                                                    1 MAPITAYAQQTRGLLGCIITSLIGSRVKNOVESEVOIVSIAAGTELATGINGVCWEVYEGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1038 ARTLAGPVGPVNCRWWSPSDDVAVYPL/PSGASCLEPCKGGTQSVWCTRN--DGALCHGRL
                                                                                                                                                                                                     .090 GNKTIAGSRGPVTQMYSSAEGDLVGWPSPPGTKSLEPCTCGAVDLYLVTRNADVIPARRR
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      Length 3033;
74.7%; Score 7.2; DH 1; Length 33
69.8%; Pred, NO, 5.4e-59;
**vo. 29; Mismatiches 26; Indels
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                                           29; Mismat.ches
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A.Molecule type: mRNA
A.Residues: 1-3005 < EKK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 33.18;
Matches 60; Conservative
                      Best Local Similarity 69.8%
Matches 127, Conservative
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probable aromatic acid decarboxylase PA4019 [imported] - Pseudomonas aeruginosa (stic) Species: Pseudomonas aeruginosa (stic) Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (stic) C;Accession: H83144  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic particle complex: A82950; MUID:20437337; PMID:10964043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Residues: 1-209 <STO>
A:Cross-references: GB:AE004816; GB:AE004691; NID:99950200; PIDN:AAG07406.1; GSP9B:(
A:Experimental source: strain PAOl
C:Genetics:
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                                                                                                                                                                                                                                                                                                                                           970 APVVVH-HHGKGFFGVVKISMTGWDETEHVGNVVVLGTSTTRSMGTCVNGVMYTTYHGSN 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1078 D--GALCHGTLGRTVELDLPAELCDFRGSSGSPILCDEGHAVGML-ISVLHRGSRVTGIR 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----YLVTRHADV1PVRRRGDSRGSLLSFR--P1S-----YLKGSSGGPLLCPA 148
A:Cross-references: BMBL:AF023424; NID:92828597; P:DN:AAC40501.1; PID:92828598
C:Superfamily: hepatitis C virus genome polyprotein
C:Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                62 TRTIASPKGPVIQMYTNVDKDLVGWPAPQGSR5LTPCTCGSSDLYLVTRHADVIPVRRKG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 SAVATGACHNIJERAADVALKER----RPLVLVPREAPFSSIHLENMLKLSNIGAVILPA 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ETDVA
                                                                                                                                                                                                                                                                          2 APITAYAQQTRGLLGCIIISLIGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 DSRGSLI.S-----PRPISYLKGSSGGPLLCPAGHAVG1FRAAVCTRG-----
                                                                                                                                                                                                         33; Caps
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                                                                                                                                         iength 2970;
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                                                                                                                                                                                                         Indels
                                                                                                                                         DB 2;
                                                                                                                                                                                                      66;
                                                                                                                                     Oucry Match 26.8%; Score 255.5; DB 2
Sest Local Similarity 30.1%; Pred. No. 1.4e-15;
Matches 59; Conservative 36; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
0.69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHAVGIFRAAVCTRGVAKAVDFIPVESLET 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angio-associated migratory cell protein - human C;Species: Homo sapiens (man)
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|1135 YTKPWETLPREAITHT 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 ftext_change 21-Jil-2000
C;Accession: 13938
R;Beckner, M.E.; Krutzsch, H.C.; Stracke, M.L.; Williams, S.T.; Callardo, J.A.; Liotta, Cancer Res. 55, 2146-2249, 1995
A;Title: Identification of a new immunoglobulin superfamily protein expressed in blood was reference number: 139383; MulD:95262124; PMID:743815
A;Reference number: 139383
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 139383
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-452 - RES.
A;Cross-references: GB:M95627; NID:q870802; PIDN:AAA68889.1; PID:q870803
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A;Genetics:
A;Map position: 14932.1-14932.1
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F;414-447/Domain: WD repeat homology <WE:>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 WTVYHGAGTRIIASPKGPVIQMYTNVDKHLVGWPAPQGSRSG-----TPCTCGSSDLYLV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 -----VLPEGKRAVVGYEDGTIRIMDLKGGSPHFVLKGTEGHEGPLICVAANODGSLILL: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 TRHADVIPVRRK---GDSRGS-----LLSPRPISYLKGSSG--GPLLGPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 WMEWH-----PRAPVLLAGT-ADGNTWAWKVPNGOCKIFOGENCFATCGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GHAVGIFR----AAVCTRGVAKAVDFIPVESL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 GSVDGQAKLVSATIGKVVGVPRPETVASQPSLGEGEBSHSNSVHSL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Indexs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

8.6%, Score 82: DB 2

Best Local Similarity 25.3%; Pred. No. 5;

Matches 42: Conservative 13; Mismatches
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Search completed: September 27, 2003, 12:22:12 Job time : 44 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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September 27, 2003, 12:28:45 ; Search time 2232 Seconds
(without alignments)
1981.817 Million coil updates/sec
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OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                   US-09-965-594-1
953
                                                                                                                                 Title:
Perfect score:
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                                              : uo
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22781392 seqs, 12152238056 residues 0.5 0.5 0.7 Xgapop 10.5 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.5 , Fgapext Delop 6.0 , Delext Searched:

BLOSUM62

Scoring table:

45562784 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20030500000

Post-processing: Minimum Match 09 Maximum Match 99% Listing first 45 summaries

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-FGAPOR-10 -XGAPOP-10 -XGAPOP-10 -XGAPOP-10 -XGAPOR-10 -XGAPOP-6

Catabase

qb\_est4:\*
qb\_est5:\*
em\_estiun:\*
em\_estom:\*
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em\_estpl:\*
em\_estro;\*
em\_htc:\*
qb\_estl:\* qb\_est2:\*
gb\_htc:\* em\_estba:\* qb\_cst3:\* 

gp\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

ipti	F304699	0892487	23748	74C64	1010	6176	33316	50999	30545	31437	53096	03244	7233	20860	9089	33286	49665	36751	98041	09745	68830	94657	5424	06661	08084	7000	04783	55608	20343	18812	37051	78418	59466	94182	26609	30299	53743	57615	7824	32604	52790	98486	
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## ALIGNMENTS

BF304699 984 bp mRNA linear FST 21-NOV-2000 6018888252F1 NIH\_MGC\_17 Homo sapiens cDNA clone IMAGE:4122276 5', Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini: Hominidae; Homo. 1 (bases 1 to 984) BF304699 BF304699.1 GI:11251586 Homo sapiens (human) mRNA sequence. RESULT 1 BF304699/c LOCUS DEFINITION ORGANISM ACCESSION KEYWORDS VERSION

REFERENCE

em\_gss\_pro: \*
em\_gss\_rod: \*
em\_gss\_rod: \*
em\_gss\_vri: \*
gb\_gssl: \*

em\_gss\_mam: em\_gss\_mus: ~

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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xrsf="laxen.ye666"
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IMAGE:6192708 5', mRNA sequence.
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                                                                                                                                                                                                                                                            found through the LA.A.S.E. Consortium/LLNZ at: image.llnl.gov
Plate: LLCM1005 row: g column: 13
High quality sequence stop: 646.
Location/Qualitiers
1. 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The ...A.A.B. Gensortium (LLNL) DNA Sequencing by: Incyte Generals, Inc. Clone distribution: MGC clone distribution can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 SerGlyGlyProbeuLeuCysProAlaGlyHisAlaValGlyTlePheArgAlaAlaVal
  NIH-MGC http://mgc.nci.sib.gov/.
National Institutes of Health, Mammalian Gene Collection (MSC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493 CGGCACGCTCCGGTCACGTGCAGC-------TTCCAGCGCCCCGGC
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22
22
52
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                     Contact: Robert Strausberg, Fh.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-965-594-1 (1-182) x BF304699 (1-984)
                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: AFCC
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454 TGCGCCGAGGA 443
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/close_lib="Lupski_sympathetic_trunk"
/close="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
No:1, Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGACCCAGGGGTCGG-3' and
5'-GACTAGTTCTAGATGGGAGGGGCGGCT(15)-3', Size selected >
1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life
Technologies.
Technologies.
362 c 343 g 211 t 28 others
                                                                                                                                                                                                                                                                                                               Conduct: Kobert Strausberg, Fil.D.

Conduct: Kobert Strausberg, Fil.D.

Email: capbs: Transionin.gov
    Tissue Procurement: Dr. James R. Lupski
    CDNA Library Preparation: Life Technologies, Inc.
    CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information on be found through the T.M.A.G.E. Consortium/LLN. at:
    http://mage.lln.gov
    Plate: LLAM13595 row: c column: 13
    High quality sequence start: 57
    High quality sequence start: 67
    // Collabiance Start: 67
    // Co
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Eukaryota; Metazoa; Chordata; Graniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                    1 (bases 1 to 1199)
NIH-MGC http://mgc.nci.nin.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/dev_stage~"adult, 16 yr"
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                                                                                                                                                                                                                                     Unpublished
Contact: Robert Strausberg, Ph.D.
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AUTHORS TITLE COURNAL

FEATURES

REFERENCE

DEFINITION

CA023748 RESULT 3

ACCESSION VERSION KEYWORDS SOURCE

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BM374064 Linear EST 23-JUL-2002 EBma03_SQ003_I16_R maternal, 8 DPA, no treatment, cv Optic, EBma63 Hordeum vulgare subsp. vulgare cDNA clone EBma03_SQ003_I16 5', mRNA
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Eukaryota: Viriciplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta: Lillepsida; Poales; Poaceae; Pooldeae
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  .89 GGAGCGCG-------GCATGTGTTTCTTCTTCTTGTTGACCAGCGGCGGCGA 236
                                                                                                                                                                                                                                                                                          97 ProCysThrCys-----GlySerSerAsp-LeuTyrLeuValThrArgHisAlaAspVa 114
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Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- GlyGluValGlnIleValSer
                                                                                                                                                                                                                                                                                                                                                           77 ThrAsnValAspLysAspLeuValGlyTrpProAlaProGlnGlySerArgSerLeuThr
                                                                                                                   30 CATCAAAIACC-ICCGGCGAGAGIIICAGCGAIAIIICIGGAGGAGGGAAGGA
                                                                                                                                                                     39 ThrAlaAlaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrpThrVal-----
                                                                                                                                                                                                                                                                 57 TyrHisGlyAlaGlyThrArgThrIleAlaSerProLysGlyProValIleGlnMetTyr
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EBma03"
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Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Genome Dynamics/Computational Biology
Genome Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotiand, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562731
Fhail: estGenisari, ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
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/mol_type-"mRNA"
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                                                                      28 AsnGlnValGlu---
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                                                                                                                                                                                                                                                                                               515 bp mRNA linear EST 23-OCT-2002
447EJ7r HZ Hordeum vulgare subsp. vulgare cDNA clone H247El7
5-PRIME, mRNA sequence.
CA023748
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Hordeum vulgare subsp. vulgare
Eukaryotta: Viridiplantae: Strephophyta: Embryophyta: Frachecphyta:
Spermatophyta: Magnoliophyta: Liliopsida: Podies: Poaceae: Fooleeae
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                                                                      yGlyProteuLeuCysProAlaGlyHisAlaValGlyIlePheArgAlaAiaValCysTh 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Radchuk,V., Zhang,H., Weschke,W., Potokina,B. and Wobus,T. Barley ESTs from developing seeds
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Grop Plant, Research (IPK)
Corressir , 7, 06466, Gatersleben, Germany
Tel: 039482-5522
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/dev_stage="0-7 DAP (days after pollination)"
/dev_stage="0-7 DAP (days after pollination)"
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Indels:
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Insert Length: 515 Std Error: 0.00
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Best Local Similarity: Query Match:

Percent Similarity:

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BASE COUNT

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            Derived from maternal Lissue dissected from developing grains (8 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptoms resources of BSSEC/SEBRAD funded cereal IGF (Investigating Gene Punction) project.
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BJ061625 MF01SSA CDNA Oryzias latipes cona cloce MF01SSA025C02 5',
Non-normalised library, directionally closed into pSPORTI.
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Perconcipha, Atherinomorpha,
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Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
Medaka EST Project in Takeda's lab
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                                                                                                                                             Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8543, Japan
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Conservative:
Mismatches:
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Contact: Tad
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Query Match:
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BJ024121 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA143D12 3', BJ024121 BJ024121
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/sex="mixture of female and male"
/tissue_type="whole embryo"
/dw_stage="seqmentation stage 20
/clone_lb="Mr01SsA cDNA"
a 166 c 165 g 144 :
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Matches:
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Oryzias latipes
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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124 ArgGlySerLeuLeuSerProArg-----ProlleSerTyrLeuLysGlySerSer 140
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Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                  1 (bases 1 to 754)
Kohara,Y., Shin-i,I., Kimura,T., Narita,T., Jindo,T. and Takeda,H.
Medaka EST Project in Takeda's lab
                                                             Euteleostomi
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                            Oryzias latipes (Japanese medaka)
Oryzias latipes
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Contact: Tadasu Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Pax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 AAAAATGACGTAGAAGGAAAAGACAGAGATGGAAGCACACATGTTGTGGGTTGTACGGGTT 361
              Kohara,Y., Shin-i,T., Kimura,T., Narita,I., Jindo,T. and Takeda,H.
Mcdaka ESI Project in Takeda's lab
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Contact: Tadasu Shin-1
Contact: Fadasu Shin-1
Contact for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-3540, Japan
Tel: 81-559-81-6855
Eax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                             /dev_stage="segmentation stage 20
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a 149 c 148 a 175 t
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                               tshini@genes.nig.ac.jp.
Location/Qualifiers
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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

RESULT 8 BF203316/c

LOCUS DEFINITION

ACCESSION KEYWORDS SOURCE

VERSION

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CB950999
AGENCOURT_13445496 NIH_MGC_177 Mus musculus cDNA clone
IMAGE:30316162 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Size fraction. Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library." 309 c 211 g 275 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 1031)
11 H-MCC http://mgc.nci.nih.gov/, National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30316162"
/lab_host="MH10B (Tl-phage-resistant)"
/clone=lib="NIH_MGC_177"
/note="forgan: liver; Vector: pDNR-LIB; Site_1: Sf:I
/note: liver; Vector: pDNR-LIB; Site_1: S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Proparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIAIL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: Plate: NCMO7 row: b column: 11
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-rèmail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
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Location/Qualifiers
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                                   166 ys 166
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/lab.host="thabdomyosarcoma"
/lab.host="thabdomyosarcoma"
/lab.host="thabdomyosarcoma"
/lab.host="thapdomyosarcoma"
/clone_lib="hTH MGC_17"
/cote="Organ: muscle; Vector: pCTB7; Site_1: EcoR1;
/site_2: XhOI: CDNA made by oliqo-dr priming.
Site_2: XhOI: CDNA made by oliqo-dr priming.
Directionally cloned into EcoR1/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubi: (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                       bF20i316
501865914F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4098578 5'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-familiah.dov
Tissue Procurement: ATC
CON Library Preparation: Linu Hong/Rubin Laboratory
CDN Library Preparation: Linu Hong.E. Consortium (LLNL)
CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNN Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found frough the I.M.A.G.E. Consortium/Lukl at: image.llnl.gov
Plate: LLCM965 rcw: I column: 03
High quality sequence stop: 637.
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Conservative:
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/mol_type-"mRNA"
/db_xref-"taxon:9605"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
Contact: Robert Strausberg, Fh.D.
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                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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BF203316
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The FANTOM Consortium and the RIKEN Genome Expicration Research Group Phase 1 & 11 Team.

Group Phase 1 & 11 Team.

Group Phase 1 & 11 Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

Bature 420, 563-573 (2002)

Seach, J. Aizawa, K. Akimura T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayaka, T., Radch, J., Ryana, J., Ryana, T., Ryana, T., Kono, H., Kouda, M., Ratch, H., Rwal, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koth, H., Kouda, M., Koth, H., Kowa, J., Konno, H., Kouda, M., Koth, H., Sakai, R., Chho, M., Ohsato, N., Ckazaki, M., Saitoh, H., Sakai, R., Shibata, K., Shibata,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gistincich, S., Hill, D., Hoffmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., whynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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/db_xref="G1:26348601"
/db_xref="G1:26348601"
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TRYGAQAQFGQRRVGACRRSEGLCLSRKPRRRQHVPPVGPHVYGLSGGRRIPPPAGE
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CDNA library was prepared and sequenced in Mouse Genome Commerced in Mouse Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="cerebellum"
/cione_lib='RIKEN full-length enriched mouse cDNA library"
/dev_stage="7 days neonate"
                                                                                                                                                                                                                                                                                                                                                        Functional annotation of a full-length mouse cDNA collection
Nature 409 (5821), 685-696 (2001)
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URL:http://geneme.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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/note="putative"
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                                                                                                                                                             ---GlnGlySerArgSerLeuThrProCysThrCysGly 101
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                                                                                     69 LysGlyProVallleGinMetTyrThrAsnValAspLysAspLeuValGlyTrpProAla 88
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Migh efficiency full-length cDNA cloning
Meth. Enzymol. 363, 19-44 (1999)
99279253
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Spermatophyta: Magneliophyta; Liliopsida, Poales, Poaceae, Pooldeae
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             /note="putative"
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109 CCCTGTTCTGCCAGGTGGCCGCGGTGGACGCGCGCGCGGGGGAGGGGGAGCGGCTCGTGGTCG 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpaqes/bgn/31/cover.html)" 216 c 311 g 105 t.
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    Dec 19, 2000 this sequence version replaced gi:11895595
                                                                                                                                                                                                                                                                                                 /organism-"Hordenm vulgare subsp. vulgare"
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Conservative:
Mismatches:
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/tissue_type="Seedling shoot"
/lab_host="TJC121"
                                                                                             SC 29634,
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/cultivar-"Morex"
/db_xref="taxon:112509"
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On Dec 19, 2000 this sequence Contact: Wing RA Clemson University Genomics In Clemson University 100 Jordar Hall, Clemson, SC 2 Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@ciemson.edu
Total hq bases = 455
                                                                                                                                                                                                                                                             Location/Qualifiers
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39.87%
30.72%
10.23%
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Db 623 ATCTITACCGGTCCGTGTCGTCTTCTACAGCTGGCTGGATCGCATCACGAACGA	: : :   : : :   : : : : : : : : : : : :	0y 78 AsnValAspLysAspLeuValGlyTrpProAlaProGlnGlyScrArgSerLeuIhrPro 97	Db 512CGGTCAITACCGCCC 498	Oy 98 CysthrCysGlySerSerAspLeuTyrLeuValThrArgHisAlaAsp 113		Qy 114 ValileProValArgArgArgGlyAspScrArgGlySerieuLcuSerProArgProIle 133		Oy 134 SerTyrLeuLysGlySerSerGlyGlyProLeuLeuCysProAlaGlyHisAlaValGly 153	is4 LiepheArgAlaAlaValCysThrArgGlyValAlaLysAlaValAsp 16 	Oy 170 PhorleProval 173 :::111111   Db 308 GGTGTTCTGTC 297	RESULT 13	DEFINITION 963042002.xl C. reinhardtii CC-1690, Stress condition 1, normalized	ACCESSION SP863244 GI:12253388	;	_	RETERENCE 1 (Dases 1 to 701) AUTHURS Grossman, A., Davies, J., Federspiel, N., Harris, E., Hauser, C.,	Integer of the Commont, J.P., Shrager, J., Siltlow, C. and Stern, D.  TILE Analyses of the Chlamydownes reinhardtii Genome: A Mode). Unicellular System for Analyzing Gene Function and Requiation in Vaccular Plants: project phase 3	COMMENT Contact: Charles Hauser COMMENT CONTEST OF THE STATES HAUSER DOWN BOX 91000 Duxe University	Durham, NC 27708-1060 Tel: 919 613 8159 Fax: 919 613 8177 Emall: chauser@duke.edu.	FEATURES Location/Qualifiers 1. 701   Source   /organism="Chlamydomonas reinhardtii"   /organism="contain"   /	/mol_type="mkNA" /strain="CC-1690 wild type mt+ 21gr" /db_xref="taxon:1055"	/Clone_lib="C. reinhardtii CC-1690, Stress condition I, normalized, Lambda 2ap II* //note="Vector: pBluescript II SK-; Site_l: ECORI; Site_2: Xho;; This library, constructed by John Davies and Jeffrey	McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP-N (30 min, lhr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, lhr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, lhr, 4hr) and NH4 to NO3 (30min, lhr, 4hr) and NHA to NO3 (30min, lh	purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda 2ap II
Qy         88 AlaproGloGlySerArgSer           1::::::::::::::::::::::::::::::::::::	104 -AspLeufyrLeuValThrArgHisAlaAspVallloProValArgAr	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	Oy 119 garqGlyAspSerArgGlySerLeuLeuSerFroArgFroIleSerTyrLeuLysGlySe 139	Db 289 CCGCGCCGTTGCCGGGGCAGTATACG-FCGCGGGGGGGCGACGACGAGGAGAACGCG 347	Oy 139 rSerGly-GlyProLeuLeuCysProAla	Db 348 crecedrodecredegracearcecearcesacecrecescocrecececercesaces 407	Oy 151 laValGiyilePheargAlaalaVa:CysThrArg 162 	Db 408 GCGGAGGAGGGGGGGGGGGGGGCTCTGCGT 442 RESULT 12	CNS09D4S/C CNS09D4S CNS09D4S E44 bp mRNA linear RIC 08-5AN-2503 DEFINITION Single read from an extremity of a fill-length cONA clone made from Anopheles gambiae total adult (emaios, 3-PRIME end of clone FKNARCNCC12 of strain 6-9 of Anotheles cambiae (African malatia	mosquire). ACCESSION BX053096 VERSION BX053096.i G1:27626377	_	ORGANISM ANOPHELES GENERAE  UNGANISM NEOPLETA: METAZOA: Arthropoda; Hexapoda; Hisecta; Flerygola;  Neopleta; Endopterydota; Diptera; Necaloceia; Clicoidea;	ATOPRELES. 1 (bases 1 to 844) AUTHORS Genoscope.	Direct Submission Submission (05-JAN-2003) Genescope - Centre National de	HP 191 91005 EVET CEGEX - FRANCE: (E-Mali: - NCb : www.gencscope.cns.fr) - Cca.lon/Qualifiers	source i 844 /organism="Anopholes gambiae"	/moi_type="mkNA" /strain="e-v" /db_xrrf="teaxon:7165" /clone="Fk0AAC90fc12"	/plasmid-"PML#5+1L". /note="end : 3-PRIME" BASE COUNT 197 a 220 c 213 g 214 t ORIGIN	29 Lengih: 96.50 Maiches:	rcent Similarity: 35.87% st Local Similarity: 23.37% ery Match:	Gaps: 3D4S (1-844)	Qy 10 GinthraigGlyLeuLeuGlyCysTleileThrSerLeuThrGlyargAspLysAsnGl:: 29 :::	Oy 30 ValGluGlyGluValGlnIleValSerThrAlaAlaGlnThrPheLeuAlaThr 47 :::	AR Cretibate (Number of the property of the pr

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846 bp mRNA linear EST 31-0C1-2000
601804028FJ NCI_CGAP_Mam5 Mus musculus cONA clone IMAGE:4035162 5',
BF182274
BF182274.1 GT:11060416
pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al. (1996) (Gnome Research 6: 791-806."
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Email: cgapbs-rāmail.pth.gov
Chrace Corder: Lothar. Lothar. Lethar. Lothar. Lethar. Let
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/mol_type="mRNA"
/strain="C57BL/63"
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BF307233 901 bp mRNA linear EST 21-NOV-2000 601891502F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4137145 5',
/db_xref-"taxon:10090"
/clone-"IMAGE:4035102"
/clone-Type-"tumor, gross tissue"
/dv_stage="Tumoths"
/lab_host-"DH10B"
/clone-lib="NCL_CGAP_Mam5"
/clone-lib="NCL_CGAP_Mam5"
/clone-lib="NCL_Comed unidirectionally, Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 lThrargHisAlaAspValIleProValArgArgArgGlyAspSerArgGlySerLeuLe 128
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Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.mih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissuo Procurement: ATCC
CDMA Library Preparation: Ling Hong/Rubin Laboratcry
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                          1 others
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/ Organism - "Homo sapiens"
// Mol_type="mkNA"
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// Mol_type="thabdomyosarcoma"
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.-AGE. Consortium/LLNL at: image.llnl.gov plate: LLCM1044 row: c column: 02
High quality sequence start: 6
High quality sequence stop: 684.
Location/Qualifiers
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Job time : 2238 secs
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Compagen Ltd.
GenCore version 5.1.6
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OM protein - nucleic search, using frame\_plus\_p2n model

September 27, 2003, 12:22:20 : Search time 327 Seconds (without alignments) 1502:446 Million cell updates/sec Run on:

US-09-965-594-1 953 Title: Perfect score:

1 MAPITAYAQQTRGLLGCIII.......GVAKAVDFIPVESLETIMKS 182 Sequence:

BLOSUM62 Scoring table:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

5105511 Total number of hits satisfying chosen parameters:

2552756 segs, 1349719017 residues

Searched:

Minimum DB seq Maximum DB seq

length: 0 length: 2000300000

Post-processing: Minimum Match 0% Maximum Match 99% Listing first 45 summaries

Database

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/SIDSI/gcqdata/qeneseq/geneseq:n-emb\_rNa1984.DAI:
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is derived by analysis of the total score distribution and

SUMMARIES

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ALIGNMENTS

AAD29795 standard; DNA; 2058 BP. AAD29795; RESULT 1 AAD29795 <u>:</u> 

HCV-1 NS3/4a mutant conformational antigen encoding DNA.

(first entry)

7-MAY-2002

Hepatitis C virus; NS3/4a antigen; HCV infection; mutant; ds.

Hepatitis C virus type 1. Synthetic. Location/Qualifiers

Key

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160

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The present invention relates to a new immunoassay solid support consisting essential; of at least one hepatitis C virus (HCV) NS3/4a conformational epitope and a multiple epitope fusion antigen (MEFA), bound to the support. The NS3/4a conformational epitope and/or MEFA reacts specifically with anti-HCV antibodies present in a biological sample from an HCV-infected individual. The immunoassay of the invention is useful for detecting hepatitis C virus infection in a biological sample. The method of the invention provides a sensitive, accurate diagnostic and prognostic tool to provide adequate patient care and to
                   161 ThrargGlyva:AlaLysAlavalAspPhelleProValGluSerLeuGluThrThrMet 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus, HCV; NS3/4a conformational epitope; seroconversion; immunoassay solid support; multiple epitope fusion antigen; MEFA; non-structural protein; gene; ds.
 121 GlyAspSerArgGlySerLeuLeuSerProArgProlleSerTyrLeuLysGlySerSer
                                                                          141 GlyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIlePheArgAlaAlaValCys
                                                                                              Immunoassay solid support, useful for detecting hepatitis C virus infection in biological sample, comprises HCV NS3/4a conformational epitope and multiple epitope fusion antigen bound to the support
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus NS3/4a conformational epitope gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product~ "HCV NS3/4a conformational epitope"
/note= "This sequence lacks a stcp codon"
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                                                                                                                                                                                                                                                                                                                                    ABK15344 standard; DNA; 2058 BP.
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02-APR-2001, 2001US-280811P.
02-APR-2001, 2001US-280867P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to hepatitis C virus (RCV) core antisen and NS (nonstructural) 3/4a antibody combination assay that can detect both HCV antigens and antibodies present in a sample using a simile solid matrix as well as immunoassay solid supports for use in the assay. The solid support is useful for detecting HCV infection in a blockgical sample. The present sequence is a DNA encoding HCV-I NS3/4a mutant conformational antigen. This sequence is used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetalaprolleThralaTyralaGlnGlnThrargGlv.cuLeuGlyCyslleTleThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyThrArgThrIlcAlaSerProLysGlyProVallleGlnMetTyrThrAsnValAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGlnIleValSerThrAla
                                                                                                                                                                                                                                                                                                  Coit D:
                                                                                                                                                                                                                                                                                                                                                                                                     Immunoassay solid support useful for detecting hepatitis C virus infection in a biological sample, comprises at least one of HCV anti-core antibody and HCV NS3/4a epitope, bound to the support
/product= "HCV-1 NS3/4a conformational antigen" /note= "CDS does not include stop codon"
                                                                                                                                                                                                                                                                                                George-Nasciemento C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2058 BP; 419 A; 634 C; 580 G; 425 T; 0 other;
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1.80
2.20
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Mismatches:
Indels:
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946.00
100.00%
98.90%
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02-APK-2001; 2001US-280811P.
02-APK-2001; 2001US-280867P.
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                                      /partial
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Medina-Selby A;
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                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP.
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                                                                                                                                                                                                                                                                                                                                                   WPI: 2002-179522/
P-PSDB; AAE18689.
                                                                          WO200196875-A2
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prevent transmission of RCV by blood and by blood products, or by personal contact. Use of NS3/4a conformational epitope in combination with MSFA, provides a sensitive and reliable method for detecting early HCV seroconversion. Use of MEKP has the added advantages of decreasing masking problems, improving sensitivity in detecting antibodies by substrate, and improving sensitivity in detecting antibodies by substrate, and improving substrate. Detection accuracy is increased and the incidence of faise results is reduced because of the identification and the use of faighty immissional might antiques within are present during the early stages of fic seroconversion. The present during the early stages of fic seroconversion. The present cutched sequence encodes the non-structural protein NSS/4a conformational epitope of the 8. LysAspLeuValGlyTrpProAlaPrcGlnGlySerArgSerJcuThrProCysThrCys 100 121 GCCCAAACCTTCCTGGCAACGTGCATCAATGGGGTGTGCTGGACTGTCTACCACGGGGC :80 24.0 GlySerSerAspirenTyrieuValThrarqHisAlaAspVallleProValArgArg 120 HILLETHIE CHILLS THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF SECOND OF THE CONTRACT OF THE GlyAspSerArgGlySerLeuLeuSerProArgProlleSerTyrLeuLysGlySerSer 140 GlyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIiePheArgAlaAlaValCys 160 GlyThrArgThrIleAlaSerProLysGlyProVallleGlnNetTyrfhrAsnValAsp 80 0 41 AlaGinThrPheLeuAlaThrCysileAsnGlyValCysTrpThrValTyrHisSlyAla 60 SerieuthrGlyargAspLysAsnGlaValGluSLyGlaValGlnIleValSerthrAla 2058 180 2 0 0 Sequence 2058 BP; 419 A; 633 C; 581 G; 425 T; 0 other; Matches: Conservative: Mismatches: Indels: Gaps: US-09-965-594-1 (1-182) x ABKI5344 (1-2058) E. ABX14410 standard; DNA; 2058 1.46e-78 946.00 100.00% 98.90% 99.27% 06-MAR-2003 (first entry) ArgSer 182 546 Similarity: AGGTCC Percent Similarity: Alignment Scores: Pred. No.: invention 23 51 14.1 161 181 541 ABX14410; 101 121 121 Best Local S Query Match: ABX14410 1D ABX1 XX AC ABX1 XX DT 06-M RESULT qq g q δ Dp. ò a ò q ò ò dC. Эb CD ò 5  $\dot{\varsigma}$ ò ò õ

The present invention relates to immunoassays comprising Hepatitis C Virus (MCV) NS3/4a conformational epicope and multiple epitope fusion antigen (MERA), bound to a solid support. The epitope and/or the multiple epitope fusion antigen react with anti-HCV antibodies present in a biological sample from an HCV-infecred individual. The immunoassays and methods of the invention are useful for detecting HCV infection in a biological sample. The inventive immunoassay solid support provides a sonsitive and reliable method for detecting early HCV seroconversion. The assays can detect HCV infection caused by any SIX known genetypes of HCV. The use of the multiple epitope fusion proteins decreases masking problems, improves sensitivity in detecting antibodies by allowing a greater number of epitopes on a unit area of substrate, and improves selectivity. The present sequence encodes HCV type I (HCV-I) NS3/4a conformational antigen, a mutant of Immunoassay solid support for detecting Hepatitis C Virus infection in biological samples, comprises Hepatitis C Virus conformational epitope ä NS3/4a conformational epitopq: multiple epitope fusion antigen; MEFA; anti-ECV antibody: NS3/4a conformational antigen; HCV infection; mutant; gene; ds. Immunoassay solid support; Hepatitis C Virus type-1; HCV-1; Tandeske L, George-Nascimento C, /product- "NS3/4a conformational antigen" /note= "This sequence lacks a stop codon" Seguence 2058 BP; 419 A; 633 C; 581 G; 425 T; 0 other; 2058 1186 2 0 0 DNA encoding HCV-1 NS3/4a conformational antigen. Matches: Conservative: Mismatches: Jength: Indels: Disclosure: Fig 3A-3D; 45pp; English and multiple epitope fusion antigen Location/Qualifiers polypeptide 1.46e-78 946.00 100.00% 98.90% 99.27% 15-JUN-2000; 2600US-212082P. 02-APR-2001; 2601US-280811P. 02-APR-2601; 2001US-280867P. 14-JUN-2001; 2001US-0881654 (GEOR/) GEORGE-NASCIMENTO (COIT/) COIT D. ø Repatitis C virus type 1. /partial 1..2058 /\*tag= ď. Arcangel P, (MEDIA) MEDINA-SELBY WPI; 2003-147573/14. ARCANGEL F. TANDESKE L. (CHIE/) CHIEN D Y. (ARCA/) ARCANGEL P (TAND/) TANDESKE L Best Local Similarity: the HCV-1 NS3/4a P-PSDB; ABG72261 US2002146685-A1. Medina-Selby A: Percent Similarity: Alignment Scores: 10-CCI-2002 Chien DY, Synthetic Query Match: 

US-09-965-594-1 (1-182) x ABX14410 (1-2058)

g ò d ò 5 ò g ò g ò a ò

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11.35 a Goodberstranged nucleoticus equinates of the Goodbers standing through clones 14i, 11b, 7f, 7e, 8h 33c, 40b, 37b, 35 a 81, 32, 33b, 25c, 14c, 8f 33f, 33g and 39c of hepatitis C virus (HCV) bonA. In creating the composite sequence the following heterogeneities were considered. Clone 33c as well as in 5 other overlapping clones, nucleotide #78g is a G. However, in clone 37b the corresponding nucleotide is an A. This heterogenity may have important ramifications for protein folding.

Conclude 33c, as well as in 5 other overlapping clones, nucleotide #78g is a G. However, in clone 37b the corresponding nucleotide is an A. This heterogenity may have important ramifications for protein folding.

Conclude 33c an A. Therefore the residue in clone 7e and in 3 other overlapping clones is an A. Therefore the residue in clone 33f is represented as a T. Conclude 1. The 3' terminal sequence of clone 33f is coverlapping clones is a T. The 3' terminal sequence of clone 33f is coverlapping clones is a T. The 3' terminal sequence of clone 33f is coverlapping clones is a T. The 3' terminal sequence of clone 33f is conclude as T. The 3' terminal sequence of clone 33f is conclude 33f and in 2 other overlapping clones is an A. The 3' terminal sequence of clone 33f and in 2 other overlapping clones is an A. The 3' terminal sequence of clone 31f and 2 other overlapping clones is an A. The 3' terminal clone 33f and 2 other overlapping clones is an A. The 3' terminal sequence of clone 3' the accuse the corresponding disucleotide in clone 3' therefore the new or clone of clone 11 is depicted and instead the overlapping of clone 3' terminal residue and instead the overlapping of clone 3' terminal residue and instead and instead the overlapping of clone 3' terminal residue and instead in corresponding incontant in configurations of multiple and instead an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the corresponding sequences in con-5'-terminal regions of multiple overlapping clones are shown. AAN92097 could be used as a source of oligomeric DNA hybridisation probes to detect the presence of HCV mucialc acids in samples. The polypeptide(s) it encodes could be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immuno- assay reagents and vaccines and to generate antibodies useful diagnosis and passive immunotherapy for HCV infection/non-A, non-B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AlaGlnThrPheLeuAlaThrCysIleAsnGlyValCysTrpThrValTyrHisGlyAla
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                                                                                                                                                                                                                                                                               is a double-stranded nucleotide sequence of the open reading frame
                                                                                                                                                                                                                                    Claim 3; Figure 26-1, 26-2, 26-3, 26-4, 26-5, 26-6; 139pp; English.
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                                                                                                                                                                                               and associated nucleic acids and polypeptide(s)
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Conservative:
Mismatches:
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88US-0271450
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100.00%
98.35%
                                                                                Kno
                                                                                                                                                                              Purified hepatitis C virus
                                                                            Houghton M, Choo QL,
                                  (CHIR ) CHIRON CORP.
                                                                                                                   WPI: 1989-159274/22
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                                                                                                                                       P-PSDB; AAP92041
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  14-NOV-1988;
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32, 33b, 25c, 14c,
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                  20
                                                         60
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                                                                                              SerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGlnIleValSerThrAla
                                                                                                                                                                          41 AlaGlnThrPhcLeuAlaThrCysIlcAsnGlyValCysTrpThrValTyrHisGlyAla
                                                                                                                                                                                                                                                      GlyThrArgThrIleAlaSerProLysGlyProVallleGlmMetTyrThrAsnValAsp
                                                                                                                                                                                                                                                                                                                                                         GlyAspSerArgGlySerLeuLeuSerProArgProIleSerTyrLeuLysGlySerSer
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            MetAlaProlleThrAlaTyrAlaGlnGlnThrArgGlyLeuLeuGlyCysTleTleThr
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86, 81,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus: HCV; non-A, non-B hepatitis; NANBH
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11 11b, 7f, 7e, 8h, 33c, 43b, 37b, 35,
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88US-0161072.
88US-0191253.
88US-0263584.
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(first entry)
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26-FEB-1988;
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02-MAR-1990
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26-OCT-1988
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to raise antibodies for immunoassay or treatment, or to produce vaccines. See also AAP90158, AAN90303-26, and AAN90328-36. (Updated on 25-MAR-2003 to correct PR field.)
                                    Sequence 5360 BP; 1060 A; 1622 C; 1532 G; 1145 T; 1 other;
                                                                                                  Indels:
                                                                                                                              US-09-965-594-1 (1-182) x AAN90327 (1-5360)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
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                                                             9,03e-78
943.00
100.00%
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                                                                               Percent Similarity:
Best Local Similarity:
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                                                     Alignment Scores:
Pred. No.:
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                                                                                                                  161 ThrangGlyValalaLysAlaValAspPhelleProValGluSerSeuGluThrThrMc: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence shows the composite cDNA sequence derived from the aligned hepatitis C virus (HCV) cDNA's in ciones 14i, 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g and 39c. The cDNA encodes antigens which react with antibodies in patients with non-A non-B hepatitis (NANRH). The cDNA can be used to design probes, or to synthesise polypeptides, which are used to diagnose HCV-induced NANBH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus gene - used for prodn. Of polynucleotide probes, polypeptide(s) and antibodies for diagnosis, prevention and treatment of infection.
                                                                                                                                                                                                                                                                                                                               Repatitis C virus: composite cDNA; probe; vaccine
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3..5360
                                                                                                                                                                                                                                                                                                              Hepatitis C virus composite probe.
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870S-0139686.
880S-0161072.
880S-0263584.
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(first entry)
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26-FEB-1988;
25-OCT-1988;
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11-NOV-1989
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GlyGlyProLeuLeuCySProAlaGlyHisAlaValGlyflePheArgAlaAlaValCyS 160
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                                                                                                                                                                                                                                                                          open reading frames of the hepatitis C virus (HCV) cDNAs from
                                                                                                                                                                                                                                             GlyThrArgThrileAlaSerProLysGlyProValIleGlnMetTyrThrAsnValAsp
                                                                                                MetalaProlleThralaTyralaGlnSlnThrargGlyLeuLeuGlyCysIleIleThr
                                                                                                                                                                                                                                                                                                                                                                  GlyAspSerArgGlySerLeuLeuSerProArgProlleSerTyrLeuLysGlySerSer
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Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                          Combined open reading frames of the hepatitis C virus (HCV) cDNAs from
               121 GlyAspScrArgGlySerLew.couSerProArgProllcScrTyrLewLysGlySerSer
                                                                                         161 ThrangGlyValAlaLysAlaValAspPhellePrcValGluSerLeuGluThrThrMet
                                                                           141 GlyGlyProf.cuLcuCysProAlaGlyHisAlaValGlyIlePheArgAlaAlaValCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7310 BP; 1491 A; 2217 C; 2058 G; 1540 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Repatitis C virus; HCV; non-A, non-B hepatitis; NANBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purified hepatitis C virus and associated nucleic acids and polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Figure 47-1 - 47-8; 139pp; English.
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                                                                                                                                                                                                                                                                                       AAN92105 standard; DNA; 7310 BP.
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87US-0139886.
88US-0161072.
88US-0191263.
88US-0263584.
88US-0271450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
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02-MAR-1990
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26-FEB-1988;
06-MAY-1988;
26-OCT-1988;
14-NOV-1988;
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AAN92106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GlyThrArqThrIleAlaSerProLysGlyProValiTleGlnMetTyrThrAsnValAsp 80
                                                                                                                                                                                                                                                                                                                                                                                                                     It is a double-stranded nucleotide sequence of the open reading frame (ORF) (tag a) extending through clones 12f to 15c of hepatitis C virus (HCV) conNa. It can be used to make oligomeric DNA hybridisation probes t detect the presence of HCV nucleida in samples. The polypeptide(s) it encodes could be used as immunoassay reagents and vaccines and to generate antibodies useful in diagnosis and passive immunotherapy for HCV incleid on 25-MAR-2003 to correct PR [ield.) (Updated on 25-MAR-2003 to correct PI field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6905 BP; 1421 A; 2082 C; 1945 G; 1456 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                              polypeptide(s)
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Matches:
Conservative:
Mismatches:
Indels:
Gups:
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                                                                                                                                                                                                                                                                                                                                                                associated nucleic acids and
                                                                                                                                                870S-0139686.
880S-0161072.
880S-0191263.
880S-0263584.
880S-0271450.
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Pred, No.:
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1128 CIGGGGCCATCACGGCGTACGCCCAGCAGAGACACACCTCCTAGGGTGCATAATCAC 1787
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                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Query Match:
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                                                                      Percent Similarity:
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19-JUL-2001
01-NOV-1989
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Alignment Scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysAspleuValG'yTrpProAlaProGlnGlySerArgSerLeuThrProCysThrCys
                                                                                                                                                                               The sequence shows a composite hepatitis C virus (HCV) cDNA, derived be aligning clones K9-1 through 15e in 5'-3' direction. The cDNA encodes antigens which react with antibodies in patients with non-B hepatitis (NANBH). The cDNA can be used to design probes, or to synthesise polypeptides, which are used to diagnose HCV-induced NANBH, to raise antibodies for immunoassay or treatment, or to produce vaccines. See also AAP90288, and AAN90333.

(N.B. This record was resulmitted to correct errors in the sequence.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polynucleotide probes, prevention and treatment
                                                                                                                                                                                                                                                                                   other
                                                                                                                                                                                                                                                                                   C; 2058 G; 1539 T; 0
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Matches:
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Indels:
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diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                       (1-7310)
                                                                                                                                                              Disclosure; fig 47; 235pp; English.
                                                                                                                       for
for
                                                                                                                                                                                                                                                                                   Sequence 7310 BP; 1495 A; 2218
                                                                                                                       Hepatitis C virus gene - used polypeptide(s) and antibodies
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87US-0122714.
87US-0139886.
88US-0161072.
88US-0263584.
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943.00
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                                                                      Choo QL,
                                                                                           WPI; 1989-215054/30.
                                                                                                                                                                                                                                                                                                                                                Similarity:
                                                                                                    P-PSDB; AAP90288
                                                   (CHIR ) CHIRON
                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
18-NOV-1987;
30-DEC-1987;
26-FEB-1988;
26-OCT-1988;
                                                                     Houghton M,
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                                                                                          LysAspleuValGlyTrpProAlaProGlnGlySerArgSerLeuThrProCysThrCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition comprising a hepatitis C virus antisense polynucleotide which is complementary to or corresponds to a sense strand of the virus genome, and selectively hybridises to it -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
viral infectivity; viral replication; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequence compiled Hepatitis C virus cDNA clones.
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/*tag= a
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89US-0341334.
89US-0355002.
90EP-0302866.
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                                                                                                                                                                                                                                                                                                                                                        2268 AGGTCC 2273
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                                                                                                                                                                                                                                                                                                                                   181 ArgSer 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
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16-MAR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus (HCV) antigens can be used for detecting HCV infected sera and individuals infected with HCV. They can also be used in an anti-HCV vaccine or for the production of anti-HCV antibodies which can be used for passive immuroprophylaxis. The antigens consistently identify more HCV positive serum samples with a high degree of specificity. See AAG98222-14 and AAR81939-51. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         of C
                                                                                                                                                                                                              Hepatitis C virus: HCV; antigen: detection; diagnosis; vaccine; antibodies; immunoprophylaxis; sera; serum; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids encoding hepatitis C virus antigens · used alop prods. for detection of HCV-infected sera and prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7310 BP; 1494 A; 2217 C; 2060 G; 1539 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
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                                                                                                        AAQ98221 standard; cDNA to mKNA; 7316 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4: Figure 11; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   develop prods. for detection of P
vaccines and anti-HCV antibodies.
                                                                                                                                                                                        Hepatitis C virus clone genome.
                                                                                                                                                                                                                                                                                                                                                                                                        Reyes GK;
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90US-0594854.
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(first entry)
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                                                111111
2268 AGGTCC 2273
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                                 181 ArgSer 182
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Best Local Similarity:
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15-AUG-1996
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Han J,
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17-SEP-1990;
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      AA207656;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises a hepatitis of virus (HCV) antisense polynucleotide. The HCV is characterized by a positive stranded RA genome which has 40% homology at the polypeptide level to a HCV polyprotein. The antisense polynucleotide binds to collular polynucleotide which enhance and/or are required for viral infectivity, replicative ability or chronicity. The antisense polynucleotides may also be designed to bind with high specificity, to be of increased stability, to be stable and to have low toxicity. The composition also comprises an agent which causes viral RAM to be luactive. The composition is used for preventing HCV cpN sequence, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AlaGinThrPheLeuAlaThrCyslleAsnGlyValCysTrpThrValTyrHisGlyAla
                                                                                                          specification describes a pharmaceutical composition which
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                                  Fig 16: 75pp; English
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Best Local Similarity:
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The invention provides two new isolates of hepatitis C virus (HCV), JI and JT. These two isolates comprise nucleotide and amino acid sequences that are distinct from the HCV isolate HCV-1. The nucleotide sequences may be used to detect non-A, non-B HCV (NANBH) polynucleotides by hybridisation for diagnosis of NANBH infections. They may also be used to screen blood donners, donnated blood and blood products for this infection. The isolates may also be used to isolate other naturally occurring variants of the virus. The polypeptides may be used as a vaccine for present sequence represents the nucleotide sequence of HCV-1 ORF.
                                                                                                                                                                                                                                                                                                                                                       /transl_except= (pos:1588..1589; aa:Leu)
/note= this codon has an apparent 1 nucleotide deletion,
which alters the reading frame.
/transl_except= (pos:1647..1650; aa:Pro)
/note= this codon has an apparent 1 nucleotide
insertion, which alters the reading frame; insertion, is not indicated in the sequence
present in the formal sequence listing of the
specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C Virus isolates, useful for diagnosis of hepatitis
                                                                                                                                      Hopatitis C virus; HCV: J1; J7; HCV-1; non-A, non-B HCV; NANBH: HCV infection; vaccine; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kolberg JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
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Mismatches:
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Weiner AJ;
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                                                                                                                                                                                                                                                                               Location/Qualifiers
268..9132
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                                                                              Nucleotide sequence of HCV-1 ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8908-0408045.
8908-0456142.
90EP-0310149.
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                                (first entry)
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(updated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-480843/41.
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Best Local Similarity:
                                                                                                                                                                                                                       Hepatitis C virus.
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US-09-965-594-1 (1-182) x AA207656 (1-9133)

AA207656 standard; DNA; 9133 BP.

AA207656 ID AA20 XX

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141 GlyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIlePheArgAlaAlaValCys 160
                                          WPI: 1990-284418/38.
                  (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                       Similarity:
                                                                                                                                                                                See also AAQ05955
                                                P-PSDB; AAR08124
                                                                                                                                                                                                                                 Percent Similarity:
     20-APR-1989;
                              Houghton M,
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                                     AlaGinThrPheLeuAlaThrCysIleAscGlyValCysIrpThrValTyrHisGlyAla
                                                                              GlyThrArgThr11eAlaSerProLysGlyProval71eGlnMetTyrThrAssvalAsp
                                                                                                                                                                                                       161 ThrArgGlyValAlaLysAlaValAspPhelleProValGluSerLeuGluThrThrMet
    MetalaprolleThralaTyralaGlnGlnThrArgGlyConLeuGlyCysileLloThr
                                                                                                                                                                                                                                                                                                                                                                                    within this region is claimed"
                                                                                                                                                                                                                                                                                                                CDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                      /note-"encodes an epitope that
                                                                                                                                                                                                                                                                                                                C virus
                                                                                                                                                                                                                                                                                                                            Hepatitis C virus (HCV); antiviral agent;
                                                                                                                                                                                                                                                                                                               Sense strand of the compiled Hepatitis
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 320..9185
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/note="epitope >
8978..9185
/*tag= c
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(first entry)
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I..1667
                                                                                                                                                                                                                                                                     standard; DNA;
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23-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 SerLeuThrGlyArgAspLysAsnGlnValGluGlyGluValGlnIleValSerThrAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEV CDNA Libraries were constructed using pooled serum from a chimpanzee with chronic HCV infection. A Lambda gtll library was screened with probes derived from previously isolated clones. The ORF is derived from the overlapping clones bilds, ag30a, CA205a, CA200a, CA216a, pi4a, CA167b, CA166b, CA84a, CA59a, K9-1, 265, 131, 121, 141, 11b, 7f, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g, 36c, 35f, 19g, 26g, 15e, b5a and 16fh. These clones extend the sequence of the HCV genome reported in EP-378216. The upstream region from nucleotides 319 to 41348 (=1.1667 in this file) is covered by clones Dilda, 18p, ag30a, CA205a, CA206a, CA206a, Andrew CA206a, CA20
                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus DNA - used for producing probes, polypeptide(s), antibodies and anti-sense polynucleotide(s) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I; 0 other;
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Mismatches:
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Matches:
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                                                                                                                                                  GlySerSerAspLeuTyrLeuValThrArgHisAlaAspValIleProValArgArgArg 120
                                                                                                                                                                                                    GlyThrArgThrIleAlaSerProLysGlyProVailleGluMetTyrThrAsnValAsp
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/note= "partial sequence; no termination codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; antisense polynucleotide;
viral infectivity; viral replication; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sense strand of HCV encoding a polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          BP.
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89US-0341334.
89US-0355002.
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/*tag= a
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P-PSDB; AAB18541.
                                                                                                                                                                                                                                                                                                               181 ArgSer 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus.
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18-MAY-1989;
16-MAR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is a hepatitis C virus (HCV) composite cDNA sequence, deduced using overlapping clones. a compass, concert the antiqenic protein encoded by this sequence is useful for detecting anti-HCV artibodies (Abs) and for screening an agent which inhibits HCV replication. A cell line infected with this virus can be used as a source of antidems. The antidem is useful for preparing vaccines for treating viral infections. See also AAQ10567.
                                                                                                                                                                                                                                                                                                                                                                                                                Cell lines infected with hepatitis C virus - are used as source of antigons for detection of HCV antibodies, for vaccines, and for screening anti-viral agents
                                                                                                                                                                                                                         virus; HCV-1; non-A, non-B hepatitis; HCV antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9185 BP: 1849 A; 2790 C; 2608 G; 1938 T; C other;
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Conservative:
Mismatches:
Indels:
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                                                                                        3935 AGGICC 3940
                                                                      Argser 182
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Best Local Similarity
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29-APR-1991
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9AQ21744
                                                             12] GlyaspSerArgGlySerLeuLeuSerProargProiteSerTyrLeuLySClySerSer 140 [1:111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] [11] 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaGlmThrPheLeuAlaThrCysIleAsnGlyValCysTrpThrValTyrHisGlyAla 60
                                                                                                                                                                           The specification describes a pharmaceutical composition which comprises a hepatitis C virus (HCV) antisense pelynucleotide. The HCV is characterized SRN genome which has 40% homology at the polypeptide level to a HCV polypection. The antisense polynucleotide binds to cellular polypudiectides which enhance and/or are required for viral intectivity, replicative ability or chronicity. The antisense polynucleotides may also be ability or chronicity. The antisense polynucleotides may also be to be stable and to have low toxicity. The composition also comprises an agent which causes viral RNA to be indective. The composition is used for preventing HCV replication in a system. The present course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 GiyGlyProLeuLeuCysProAlaGlyHisAlaValGlyIlePhcArgAlaAlaValCys
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                             polynucleotide which is complementary to or corresponds to a sonse
strand of the virus genome, and selectively hybridises to it
Novel composition comprising a hepatitis C virus antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9185 BP; 1849 A; 2790 C; 2508 G; 1938 T; 0 other;
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Conservative:
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900S-0565209
                                                  Cheo QI,
                         (CHIR.) CHIRON CORP
10-AUG-1990;
                                                 Houghton M.
Kolberg JA:
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Weiner AJ, Uredea MS, Kuo G,

Irvine BD:

WPI; 1992-080094/10. P-PSDB; AAR21519.

Reagents for isolating, amplifying and detecting ECV polynucleotide(s) - used to monitor spread of blood-borne non-A, non-B hepatitis virus infection and screen blood samples for

Disclosure, Fig 1; 67pp; English

The sequence is a composite of ECV cDNA from HCV1, a prototypic HCV. The sequence is based upon sequence information derived from a no. of HCV cDNA clones, which were isolated form a no. of HCV cDNA libraries, including the "c" library prosent in lambda quill complete, including the "c" library prosent in lambda quill complete, and from human serum. The HCV cDNA clones were isolated by mothods described in WO9014436.

The clones from Which the sequence was derived are Sclone32, The clones from Which the sequence was derived are Sclone32, chala, 18a, ag30a, CA205a, CA290a, CA216a, pil4a, CA167b, CA156e, chala, 18a, ag30a, CA50a, WF-1 (also called K9-1), 256, llt, 64 and pillift, 14a, 84, 334, 334, 339, 256, llt, 256, llt, 256, llt, 18a, 16jh, 6k and pillift, 14a, 84, 334, 334, 334, 256, llt, 256, (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct P1 field.) 

Sequence 9400 BP: 1885 A: 2860 C: 2671 G: 1964 T: 0 other:

Conservative: Mismatches: Length: Matches: Indels: Gaps: 1,81c-77 943.00 100.008 98.358 99.958 Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

US-09-965-594-1 (1-182) x AAQ21744 (1-9400)

81 LysaspleuValGlyTrpProAlaProGlnG.ySerArgSerLeuThrProCysThrCys 100 101 GlySerSerAspLeuTyrLeuValThrArgHisAlaAspVallleProValArgArgArg 120 5 q qq qc ô g οý ò ć ò οχ

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        GenCore version 5.1.6
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TVCARAZAPPPSWDGWCLI, HLKPTLHGPTPILY RLGAVQNEITLHPVTKY YMTCM
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Immunoassays for anti-hev antibodies
Patent: Wo 0196670-A i 20-DEC-2001:
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Patent: WO 195675-A. 2. 20-DEC-2001;
CHIRON CORPORATION (US)
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AX395309
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PAT 06-JUL-2002

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Submitted (69-APR-2001) Infectious Disease Research, Henry Ford
Health Systems, 2799 W. Grand Blvd. Rm 7845 E.s. R. Detroit, M.
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Holland-Staley,C.A., Kovari,L.C., Golonberg,E.M., Pobursky,K.J.
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Holland-Staley, C.A., Kovari, L.C., Colomberg, E. and Mayers, D.L.
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                                          Pobursky, K.J.
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Submitted (09-ARR-2001) Infectious Disease Research, Henry Ford
Health Systems, 2799 W. Grand Bivd. Rm 7045 E 8 R. Detroit, NT
48202, USA
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Helland-Staley,C.A., Kovari,i.C., Golenberg,E.M.,
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/mol type-"genomic RNA"
/isolate-"bt.lr"
/db.xref="taxon:11131"
/note-"type: 1A"
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/protein_id="AAK54560.1"
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NANBW diagnostics and vaccines
Patent: US 6150087-A 53 21-NOV-2000;
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Houghton,M., Choo,O.-K.
Patent: WC 8904669-A 8 0
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Houghton,M., Choo.Q.-L. and Kuo.G.

Nanby diagnostics and vaccines

Patent: EP 0318216-Al 48 31-MAY-1989;

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from Patent EP 0318216.
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NANBY diagnostics and vaccines
Patent: US 6150087-A 65 21:NOV-2600;
Location/Qualitiers
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Houghton,M., Choo,Q.-L. and Kuo,G.
Nanby diagnostics and vaccines
Patent: EP 0318216-A1 54 31-MAY-1989;
Location/Qualifiers
1. 6785
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Matches:
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Choo, 0.-L., Richman, K. and Ham, J.
The nucleotide sequence of the Hepatitis C viral genome Unpublished (1990)
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Houghton,M., Choo,Q.-K. and Kuc,G.
Patent: WO 8904669-A 15 01-JCN-1989;
Location/Qualifiers
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ILOASLLKVPYFVRYOGLLRFCALARKMIGHYVQMY11KIGAL;GTVYYNHLTPLRD
KAHNGLRDLAVAVEPVVFSQMETKI.TWGADTAACGDIINGLPVSARRGREILLGPAD
GWASKGKRLLAPITAYAQYDIRGLICGITSLIGRBKNQVGBGSVQIVSTAAQTFLACI
NGVCMYVYHOAGITH ASPKGPV1OMTNWDQILVGPRAPQGSRSLTPCITGSSSDLYL
VTRHADVIPVRRGDSRGSLLSPRP1SYLKGSSGGPLICPAGHAVGIFRAAVCTRGVA
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FVGAGLAGAAIGSVGLGKVLIDILAGYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAI
LSPGALVYCVCAALIRRHVGPGEGAVQMANELIAFASRGNWYSPTHYVESDAARV
LATLSSLTVGTVCLIRRLHQUISSECTTPCGSWILRDINDWICEVLSDFKTWLKAKLMPQ
LIPQIPFYSCORGYKWWRVDGIMHTRCHCGAEITGHVKNGTMRIVGRATCRNMASGTF
PINAYTIGPCTPLPAPNYTFALMRVSAEEYVEIRQVGDFHYVTGMTDNLKCDCQVPS
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AAMETARHTPVNSWLGNIIMFAPTLWARMILMTHFFSVEIARDQLEQALDCEIYGACY
SIEPLDLPPIIQRE"
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YNPPLVETWKKPDYEPPVVHGCPLPPPKSPPVPPPRKKRTVVLTESTLSTALAELATR
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SSEANAEDVVCCSMSYSWTGALVTPCAAEEQKLPINALSNSLLFHHNLVYSTTSRSAC
QRQKKVTFDRLQVLDSHYQDVLKEVKAAASKVKANLLSVEEACSLTPPHSAKSKFGYG
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GTVPAKSVCGPVYCFTPSPVVVGTTDRSGAPTYSWGENDTDVFVLNNTRPPLGNWFGC
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text: Hepatitis C virus, cDNA to viral RNA, clones, isolated from chimpanzee (individual 910) blood
                                                                  plasma.

Draft entry and printed sequence for [1] kindly submitted by M.Houghton, 22-FEB-1990. Chiron Corporation, 4560 Horton Street, Emeryville CA 94608
Original source text: Hepatitis C virus, CDNA to viral
K9-1 through 15e, isolated from chimpanzee (individual
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/mol_type="genomic RNA"
/db_xref="taxon:11103"
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                                 4) AladinThrpheLeuAlaThrCysileAsnGlyValCysTrpThrValTyrHisGlyAla
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Sequence 137 from patent US 6150087.
AR118726 GI:14100638
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Chich, D.Y.
NANBV diagnostics and vaccines
Patent: US 6150087-A 137 21-NOV-2000;
Location/Qualifiers
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Patent: US 6150087-A 88 21-NOV-2060;
Location/Qualifiers
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Chien, D.Y.
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"Genetic Diversity and response to The NS3 Protease Gene from
Clinical Strains of the Hopatitis C Virus.";
Submitted (APR-2001) to the EMBL/GenHank/DDRU databases.
EMBLA PR96219, ARAS5443.1;
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SEQUENCE
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61 GIRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRSJJPCTCGSSDLYLVTRHADVIPVRRR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQIFLATCINGVCWIVYHGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.
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Hepacivirus.
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98.4%; Pred. No. 7.1e-87;
live 3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2436 2436
2436 AA: 264734 MW: LTB9872900BB3125 CRU64;
(MAY-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 3011 AA
                                                                                                                                                                                                                                                                               IPR001650; Helicase_C.
IPR007095; RNA_pol_DS_PS.
IPR0C7094; RNA_pol_PSvir.
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J. Gen. Virol. 82:1291-1297(2001).
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                                                                                                                                                                                                    IPR001490; HCV_NS4b.
IPR002868; HCV_NS5a.
IPR002166; HCV_RdRP.
                                                                                              interPro; IPR00253;; HCV_NSI.
InterPro; IPR002518; HCV_NS2.
InterPro; IPR006109; HCV_NS3.
InterPro; IPR006745; HCV_NS4a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam: PF01506; HCV_NS5a; 1.
Pfam: PF00271; Helicase_C; 1.
Pfam: PF00999; Viral_RGRP; ProDom: PD186062; HCV_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                     Pfam: PF01560; HCV_NS1: 1.
Pfam: PF01538; HCV_NS2: 1.
Pfam: PF02907; HCV_NS3: 1.
Pfam: PF01006; HCV_NS4a: 1.
Pfam: PF01001; HCV_NS4b: 1.
                     EMBL; M32084; AAA45677.1;
HSSP; P27958; 1A1V.
                                                                           IPR001410; DEAD
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Matches 179; Conservative
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RS 757
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DSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR 181
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                                                                                                                                                                                      STRAIN-PL.4B:
Holland-Staley C.A., Kovati L.C., Golenberg E., Mayers D.L.:
Genetic Diversity and response to IFN of the NS3 Protease Gene from
Cinnoal Strains of the Hepatitis C Virus.':
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR369240; AR84565.1;
DitterPro: IPR004109; HCV NS3.
Pfam: PF02907; HCV_NS3: I.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF362223. AAK54557.1;
InterPro; IPR004109; HCV_NS3.
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19114 NW: ABB90B5B3ABA4E26 CRC64;
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181 AA: 19115 MW; 5D85F88AD7AC1A11 CRC64;
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Last annotation update)
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Pred. No. 3.8e-88;
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98.9%;
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01-DEC-2001 (IXEMBLE) 19,
01-MAR-2003 (IXEMBLE) 23,
NG3 prolease (Fragment).
Hepaills C virus.
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Best Local Similarity 98.9°
Matches 179; Conservative
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Matches 179, Conservative
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NCBL_TaxID=11103;
                  Hepacivirus.
NCBL_TaxID=11103;
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SEQUENCE
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Q91RS1
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PROSITE; PSC0190: CYTOCHRONE_C: 1.
PROSITE; PSC0190: CYTOCHRONE_C: 1.
PROSITE; PSC0507; RDRP_VIRAL; 1.
ATP-binding: Coat: protein; Bivelope protein; Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
-:- SCBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELORE CONSISTS OF TWO PROTEINS:
PROTEIN AND GIYCOPROTEIN B. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA (BY SIMILARITY).

FROTEIN C AND MRNA (BY SIMILARITY).

FROTEIN AF211632: AAF81759.1: -.

HSSP: P27958: 1AIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0: Indels
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Last sequence update)
Last annotation update)
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InterProj irrollendining.
InterProj irrollendining.
InterProj IPR001169; HCV_NS5.
InterProj IPR001469; HCV_NS5.
InterProj IPR001469; HCV_NS4.
InterProj IPR001469; HCV_NS5.
InterProj IPR001469; HCV_NS5.
InterProj IPR001659; HAZ_POL_DS_FS.
InterProj IPR001969; RNA_POL_DS_FS.
InterProj IPR007094; RNA_POL_DS_FS.
InterProj IPR007094; RNA_POL_DS_FS.
InterProj IPR007094; HCV_Core; J.
Pfam; PF011543; HCV_Core; J.
Pfam; PF011543; HCV_Core; J.
Pfam; PF011560; HCV_NS1; J.
Pfam; PF01006; HCV_NS3; J.
Pfam; PF01006; HCV_NS4; J.
Pfam; PF01006; HCV_NS4; J.
Pfam; PF01006; HCV_NS4; J.
Pfam; PF01006; HCV_NS4; J.
Pfam; PF00106; HCV_NS4; J.
Pfam; PF00106; HCV_NS4; J.
Pfam; PF00106; HCV_NS5; J.
Pfam; PF00106; HCV_NS5; J.
Pfam; PF00106; HCV_NS5; J.
Pfam; PF00106; HCV_NS5; J.
                                                                                                                                                                                                                                                                 interprovides 19800345; Cytc_hemc_bind.
Interprovides 19800416; DEAD.
Interprovides 19800525; HCV_capsid.
Interprovides 198002521; HCV_core.
Interprovides 198002519; HCV_core.
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01-DEC-2001 (TEMBLE) 19.
01-MAK-2003 (TEMBLE) 23.
NOS3 Protease (Fragment).
Hepatitis C virus.
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RS 1207
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51 TRIASPREPATOMYTNVDKDINGWPAPQCARSLIPCTGGSSDLYLVTRHADVIPVRRG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 DSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDF1PVESLETTMR
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                                                                 STRAIN-PL.61;
Holland-Staley C.A., Kovari L.C., Golenberg E., Mayers D.L.;
Holland-Staley C.A., Kovari L.C., Golenberg E., Mayers D.L.;
"Genetic Diversity and response to IFN of the NS3 Protease Gene from
"Ginical Strains of the Hepatitis C Virus.";
Submitted (APR-201) to the EMBL/Genbank/DDBJ databases.
EMBL; AF36922; AAK54547.1;
InterPro; IPR004109; HCV_NS3;
Pfam; PF02907; HCV_NS3; 1.
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"Genetic Diversity and response to IFN of the NB3 Protease Gene from Clinical Strains of the Hepatitis C Virus.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
FiNBL. AF862237; AR854652.1;
InterPro: IPR004109; HCV_NS3.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
NS3 protease (Frament).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 181;
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98.3%; Pred. No. 6e-88;
tive 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             181 181
181 AA: 19114 MW: ABB90B5B3ABA4E26 CRC64;
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181 AA: 19101 MW; 614ADABBOF33CCAF CRC64;
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98.9%; Pred. No. 3.8e-88;
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   [1]
SEQUENCE FROM N.A.
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                                          TRIBASPKGPVIQMYINVDKDLVGMPAPQGSKSLTRCTCGSSDLYLVTRHADVIPVRRG 121
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181 AA: 19144 MW: COC91F1528EB0532 CRC64;
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01-DEC-2001 (TrEMBLICL, 19, Last sequence update)
01-MAR-2003 (TrEMBLICL, 23, Last annotation update)
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01-DEC-2001 (TramBirel, 19, Last sequence update)
01-MAR-2003 (TramBirel, 23, Last annotation update)
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Matches 179; Conservative
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Hepatitis C virus.
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Hepatitis C virus.
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Okamoto H., Okada S., Sugiyama Y., Kurai K., Iizuka H., Machida A.,
Okamoto H., Okada S., Sugiyama Y., Kurai K., Iizuka H., Machida A.,
Miyakawa Y., Mayuni M.,
Miyakawa Y., Mayuni S.,
Miyoleotide sequences of the genomic RNA of hepatitis C virus isolated
from a human carrier: comparison with reported isolates for conserved
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                                          Holland-Staley C.A., Kovari L.C., Golenberg E., Mayers D.L.; "Grontic Diversity and response to Thr of the NS3 Protease Gene from Clinical Strains of the Hepathiis C Virus."; Submitted (APK-2001) to the EMBL/GenBank/DDBJ databases. EMBL, APSG-203, AAK54555.1; "Inturpro, IPR004109; HCV_NS3.
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MEDLINE=93117120; PubMed-1335573;
Oxamoto H., Kanai N., Mishiro S.;
"Full-length nucleotide sequence of a Japanese hepatitis C virus isolate (HC-JI) with high homology to USA isolates.";
Nucleic Acids Res. 20:6410-6410(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 939; DB 12; Longth 181;
Pred, No. 7.6e-88;
3; Mismatches 0; Indels 0
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Okamoto H., Okada S., Sugiyama Y., Yotsumoto S., Tanaka T.,
Yoshizawa H.;
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181 181
181 AA: 19132 WW, 0BB90B5F3AB95250 CRC64;
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01-NOV-1996 (TIEMBLEEL. 01, Last sequence update)
01-MAR-2003 (TIEMBLEEL. 23, Last annotation update)
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses,
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J. Gen. Virol. 72:2697-2704(1991).
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Best Local Similarity 98.3%;
Matches 178; Conservative
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                                                                                                                                          12. DSRGSLLSPRDISYLKGSSGGPLLCPAGHAVGTFRAAVCTRGVAKAVEFFPVESLETTMF 180
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                                                                                               122 DSRGSLLSPRPISYLKGSSGGPLLCDAGHAVGIFRAAVCTRGVAKAVDFIDVESLETTMR
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Hepacivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        991RS9 PRELIMINARY, PAGE CONTROL OF DESCRIPTION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
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Pred. No. 6e-88;
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98.9%;
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es 179; Conservative
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Hepatitis C virus.
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                                                                                                                                                                     1 MAPITAYAQOTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PSSUSUY, NEWLY, 1, PROSITE: PSSUSSIY, SURPLY II. ATP-binding; Coat protein; Enve; ope protein; Glycoprotein; Hydrolase; Nonstructural protein; Polyprotein; Hydrolase; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                              Mink M., Benichou S., Madaule P., Tiollais F., Prince A.,
                                                      to the EMBL/GenBank/DDBC databases
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                                                                                                                            MEDLINE=94174722; PubMed-7510436;
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Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00271; hclicase_c; 1.
Pfam; PF00998; viral_RGRP; 1.
ProDom; PD186062; HCV_NS1; 1.
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                                   Okamoto H.;
Submitted (DEC-1992)
                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                              Inchauspe G.
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STRAIN-Pt.176;

Holland-Staley C.A., Kovari L.C., Golenberg E., Mayers D.L.;

Holland-Staley C.A., Rovari L.C., Golenberg E., Mayers D.L.;

Genetic Diversity and response to IFN of the NS3 Protease Gene from Clinical Strains of the Hepatitis C Virus.;

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, A7369225; AAK54550.1;

FinterPro; IPR004109; HCV_NS3.

Pfam: PF02907; HCV_NS3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holland-Stalley C.A., Kovari L.C., Golenberg E., Mayers D.L.;
"Generic Diversity and response to IrN of the NS3 Protease Gene from
"Generic Diversity and response to IrN of the NS3 Protease Gene from
Clinical Strains of the Hepatitis C Virus.";
Submitted (APR-2001) to the EMBL/GenRank/DDBJ databases.
EMBI. APR6519; AAK55494 1;
InterPro. IPR064109; HCV_NS3.
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                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                    091RT4;
21-DEC-2001 (TIEMBLREL. 19, Created)
21-DEC-2001 (TIEMBLREL. 19, Last sequence update)
CI-MAR-2003 (TIEMBLREL. 23, Last annotation update)
NS3 protease (Fragment).
Hepatitis C virus.
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Last annotation update)
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3: Mismatches
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091RS8;
091RS8;
01-DEC-2001 (TFFMBLrel. 19, Created)
01-DEC-2001 (TFFMBLrel. 19, Last sequen
01-MAR-2003 (TFEMBLrel. 23, Last annotte
NS3 protease (Fragment)
Hepatitis C virus.
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Matches 178; Conservative
PRELIMINARY;
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181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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NCBL_TaxID=11103;
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Holland-Staley C.A., Kovari L.C., Golenberg E., Mayers D.L.;
Holland-Staley C.A., Kovari L.C., Golenberg E., Mayers D.L.;
Genetic Diversity and response to The of the NS; Protease Gene from
"Clinical Strains of the Hepatitis C Virus";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF369220; AAK5445.1;
InterPro; IPRO64109; HCV_NS3.
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Search completed: September 27, 2003, 12:21:21

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AAR31621 AAR90931

AAW34480 AAW4C038 AAE22049 AAU84597 AAE21847 AAE19905

Hepatitis C virus Hepatitis C virus

Peptide encoded by Protein encoded by Composite hepatiti polyprotein

AAP90288 AAB18540 AAR34609 AAR70230

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Hepatitis C virus; NS3/4a antigen; HCV infection; mutant; mutein.
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(first entry)

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HCV polyprotein.
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AAE21843 AAE21844

AAE21839 AAE21838 AAE21840 1841

AAE2! AAE21 AAE21845 AAE21846 AAE19900 AAE19907 AAE19908 AAE19919

/note- "Wild type Thr substituted with Pro" .ccation/Qualifiers 15-JUN-2000; 2000US-212682P. 62-APR-2001; 2001US-280811P. 02-APR-2001; 2001US-280867P. 14.JUN-2001; 2001WO-US19369 /note-404 (CHIR ) CHIRON CORP Misc-difference WO200196875-A2 20-DEC-2001 Hepatitis C virus HCV-: NS3/4a confo HCV genomic amino Hepatitis C virus Protein sequence o Peptide encoded by Sequence encoded i Sequence encoded i HCV-1 NS3/4a mutan

AAU76377 ABG72261 AAR40120 AAR51170 AAP92041 AAP90158 AAP90164

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                                                                                                                                                                                                                                                                                                                                                                                          GIRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRSLIPCTGGSSDLYLVTRHADVIPVRRR 120
                                                                                                                                                                                                                                                                                                                                                                                                        ODSRGSLLISPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTM 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GESRGSLLSPRPISYLKGSSGGPLLCPAGERAAUTRGVAKAVDETPVENDETTH 16
                                                                                                                                                                                                                                                                                                                                                     The present invention relates to hepatitis C virus (ECV) core antiger and NS (nonstructural) 3/4a antibody combination assay that can detect both HCV antigens and antibody especin in a sample using a single solid matrix as well as immunoassay solid supports for use in the assay. The solid support is useful for detecting HCV infection in a biological sample. The present sequence is HCV-1 NS3/4a mutant conformational antigen. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus: HCV: NS3/4a conformational epitope; seroconversion; immunoassay solid support; multiple epitope fusion antigen; MEFA; non-structural protein; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                        1 MAPITAYAQQTRGLIGGIITSIIGRDKNQVEGHVQIVSTAAQTFLATGINGVCRTVYHGA
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus NS3/4a conformational epitope protein sequence.
          Coit
                                                                                 support useful for detecting hepatitis C virus
                                                                                                infection in a biological sample, comprises at least one of HCV anti-core antibody and HCV NS3/4a epitope, hound to the support
                                                                                                                                                                                                                                                                                        Length 686;
          George-Nasciemento C,
                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Wild-type Thr substituted by Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Wild-type Ser substituted by Ile"
                                                                                                                                                                                                                                                                                      Score 946; DB 23;
Pred. No. 1.20-89;
2; Mismatches 0:
          Tandeske L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU76377 standard; Protein: 686 AA
                                                                                                                                      Example 2; Fig 4; 87pp; English.
                                                                                                                                                                                                                                                                                      99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2001; 2001WO-US19156
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                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.9
Matches 180: Conservative
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          Arcangel P,
                                              WP1; 2002-179522/23.
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                                                                                                                                                                                                                                                              686 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
Synthetic.
                                                                                    Immunoassay solid
                                                            N-PSDB; AAD29795
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                      Medina-Selby A;
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          汉,
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                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                          9
          Chien
                                                                                                                                                                                                                                                                                                                Matches
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The present invention relates to a new immunoassay solid support

consisting essentially of at least one hepatitis C virus (HCV) NS3/4a

conformational epitope and a multiple epitope fusion antique. (MEPA).

bound to the support. The NS3/4a conformational epitope and/or

MEPA reacts specifically with anti-HCV antibodies present in a biological

sample from an HCV-intected individual. The immunoassay of the invention

is useful for defecting hepatitis C virus infection in a biological

sample. The method of the invention provides a sensitive, accurate

diagnostic and progressic tool to provide adequate patient care and to

prevent transmission of uro by blood and by blood products, or by

personal contact. Use of NS3/4a conformational epitope in combination

with MEPA, provides a sensitive and reliable method for detecting early

SC seroconversion. Use of MEPA has the added advantages of decreasing

masking problems, improving sensitivity in detecting antibodies by

substrate, and improving substrate. Detection accuracy is increased and

the incidence of false results is reduced because of the identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GTRTIASPKGPVIQMYINVDKDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and the use of highly immunogenic HCV antigens which are present during the early stages of HCV seroconversion. The present amino acid sequence represents the non-structural pretein NS3/4a conformational epitope of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAPITAYAQQTRGLLGCIIISLTGRDKNQVEGEVQ;VSTAAQTFLAICINGVCWTVYHGA
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                                                                                                                                                                                                                                                                                                                                                      Immunoassay solid support, useful for detecting hepatitis C virus infection in biological sample, comprises HCV NS3/4a conformational epitope and multiple epitope fusion antigen bound to the support
                                                                                                                                                                              Coit D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.3%; Score 946; DB 23; Length 6 98.9%; Pred, No. 1.2e-89; Live 2; Mismatches 0; Indels
                                                                                                                                                                              Tandeske L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV-1 NS3/4a conformational antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 3: 92pp; English.
:5-JUN-2000; 2000US-212082P.
02-APR-2061; 2001US-280811P.
02-APR-2001; 2001US-280867P.
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N-PSDB; ABK15344.
                                                                                                                                                                                 Arcangel
                                                                                                                      (CHIR ) CHIRON CORP
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Best Local Similarity
Matches 180; Conserv
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| RS 182
                                                                                                                                                                              Chien DY, Arcar
Medina-selby A;
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Mon Sep 29

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The present invention relates to immunoassays comprising Hepatitis 2 Virus (HCV) NS34a conformational epitope and multiple epitope [usion antigen (MEFA), bound to a solid support. The NS3/4a epitope and/or the miltiple epitope fusion antigen react with anti-HCV antibolies present in a biological sample from an HCV-infected individual. The immunoassays and methods of the invention are useful for detecting HCV infection in a biological sample. The inventior are useful or detecting early HCV seroconversion. The assays can defect HCV infection anased by any CK seroconversion. The assays can defect HCV infection caused by any contains decreases masking problems, improves sensitivity in detecting antibodies by allowing a greater number of opiopes on a unit area of substrate, and improves selectivity. The present sequence represents HCV type 1 (9CV-1) NS3/4a conformational antidee, a mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoassay solid support for detecting Hepatitis C Virus infection in
biological samples, comprises Hepatitis C Virus conformational epitope
and multiple epitope fusion antigen
                                                                                                                                                            "Corresponds to amino acid residues 1027-1711 of HCV-1 NS3/4a polypoptide"
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Immunoassay solid support; Hepatitis C Virus type-1; HCV-1; NS3Aa conformational optupe; multiple epitopo islon aution; MEFA; anti-HCV antibody; NS3Aa conformational autique; HCV infection; mutent; mutekin
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                                                                                                                                                                                                           /note- "Substitution of wild-type Thr
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                                                                                                                                 Location/Qualifiers
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2001US-280811P.
2001US-280857P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIE/) CHIEN D Y.
(ARCA/) ARCANGEL P.
(TAND/) TANDESKE J.
(GEOR/) GEDRGE-NASCIMENTO C.
(COII/) COIT D.
                                                                                                                                                                                                                                                                                                                                        14-JUN-2001: 2001US-0881654
                                                                                Hepatitis C virus type 1. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arcangel P,
                                                                                                                                                              /note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MEDI/) MEDINA-SELBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-147573/14.
                                                                                                                                                                                              Misc-difference 403
                                                                                                                                                                                                                              Misc-difference 404
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                                                                                                                                                                                                                                                                            US2002146585-A1
                                                                                                                                                                                                                                                                                                                                                                                         02-APR-2001:
02-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2000;
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                                         61 GTRTIASPKGPV1QMYTNVDQDLVGWPAPQGSRSLTPCTGGSSDLYLVTRHADVIPVRRR 120
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                          GUSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNA was isolated from the plasma of a HCV scropositive human (designated "IG") and cDNA was prepared from it. The CDNA was PCR amplified using specific primers with sequences based on the prototype HCV-1 CDNA sequence (GENBANK M6232). Further amplification using nested primers resulted in 7 adjacent HCV DNA fragments which could be assembled into a full-length sequence. The DNA sequence was determined and translated into the genomic amino acid sequence.
                                                                                                                                                                                                                                                                      HCV genomic amino ucid sequence isolated from infected human LG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New plasmid pHCV-162 is a mammailan expression systems for HCVD proteins - useful for diagnosing HCV infection and as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 944; DB 14; Length 3011;
Pred. No. 1.4e-88;
3; Mismatches 0; Indeis 0
                                                                                                                                                                                                                                                                                               Hepatitis C Virus; Non-A, non-B hepatitis Virus; HCV; NANBHV; human growth hormone; HGH; secretion signal; fusion protein;
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                                                                                                                                                                           AAR40120 standard; Protein: 3011 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for preventing HCV infection
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98.4%;
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                                                                                                                                                                                                                                 (updated)
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                                                                                                                                                                                                                                                                                                                                                       Hepatitis C Virus.
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|RS 182
                                                                                RS 182
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27-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamaguchi
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Indels

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Dength 685

99.3%; Score 346; DB 24; 98.9%; Pred. No. 1.2e-85; 2; Mismatches

Matches 180; Conservative

δ g δ

Best Local Similarity

Query Match

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EP318216-A.
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.086 GTRTIASPKSPVIQMYINVDRDLVGWPAPQGARSTIFFCTGGSSDLFLVTRHADVIPVRRR 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GDSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIFVBSLETTM 196 (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (11111) (1111) (1111) (1111) (111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide fragments of the non-structural protein (NSA) are reactive with and can detect antibodies against the NSA domain of ECV. The peptides can be used for diagnosis of ECV infection. Nonspecific reaction can be inhibited and misdiagnosis of ECV intection can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptido(s) roactive with acti-hepatitis C virus actibody specific, early diagnosis of MCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide, antibody; hepatitis C virus; HCV; identilication; diagnosis; non-A non-B hepatitis; NANB; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0: indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 943; DB 15;
Pred. No. 2.1c-89;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus non-structural protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure: Page 9-10: 15pp: Japanese
                                                                                                                                                                                                                                                                   Ž
                                                                                                                                                                                                                                                               poptide: 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OLYU ) OLYMPUS OPTICAL CO LTB.
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98.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92JP-0209201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        See AAR51162-70.
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 98.4 Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 1994-106803/13.
                                                                                                                                                                                                                                                                 AAR51170 standard:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               609 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
                                                                                                                                                             RS 1207
                                                                                                                       KS 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP06056891-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                20-0C1-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        decreased.
                                                                                                                                                             1206
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                                                                                                                                                                                                                                                                                                         AAR51170;
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It is the sequence encoded in the open reading frame of hepatitis C virus coba inserts in clones 141,m 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 81, 32, 33b, 25c, 14c, 8f, a3f, and 3gc, 1t is antiqenic and could be used in immunoassay reagents and vaccines and to generate antibodies useful in diagnosis and passive immunotherapy for HCV infection/non-A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GTRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                    Seguence encoded in the hepatitis C virus (HCV) cDNA inserts in clones 141, 11b, 7f, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g and 39c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAPITAYAQQTRGLLGCIITSLTGRDKNQVEGEVÇIVSTAAQTFLATCINGVCWTVYHGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Figure 26-1, 26-2, 26-3, 26-4, 26-5, 26-6, 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                indels
                                                                                                                                                                                                                                                       Hepatitis C virus (HCV); non-A, non-B hepatitis (HANBH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and associated nucleic acids and polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.0%; Score 943; DB 10;
98.4%; Pred. No. 6.8e-89;
tive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
AAF92041 standard; protein; 1766 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    870S-0122714.
870S-0139886.
88US-0161072.
88US-0191263.
88US-0263584.
86US-0271450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIIC G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 98.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             88EP-0310922
                                                                                            (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parified hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton M, Choo Q1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1989-159274/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1766 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Watches 179; Conserv
                                                                                                                                                                                                                                                                                                     Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAN92097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful in diagno
non-3 hepatitis.
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RS 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-1588;
                                                                                         25-MAR-2003
02-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1987;
26-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-1989
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18-NOV-1988; 18-NOV-1987;

GB2212511-A 26-JUL-1989

25-MAR: 2003 10-NCV-1989

AAP90158;

RESULT 7 AAP90158 Houghton M,

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Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDSRGSLLSPRP;SYLKGSSGGPLLCPAGHAVG!FRAAVCTRGVAKAVDFIPVESLETTM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoded in the hepatitis C virus (HCV) cDNA inserts in clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is the peptide encoded by the composite hepatitis C virus (HCV) CDNA of AAN90331. The polypeptides are used to diagnose HCV induced NANBH, to raise antibodies for immunoassay or treatment, or to produce vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus qune - used for produ. of polynucleotide probes, polypeptide(s) and antibodies for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                     Hepatitis C virus; clone 121; clone 15e; probe; vaccine
                                                                                                                                                    Peptide encoded by composite hepatitis C virus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; fig 32; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuo G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-0122714.
87US-0139886.
88US-0161072.
86US-0263584.
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                                                                            (first entry)
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Best Local Similarity 98.45
Matches 179; Conservative
                             (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPi; 1989-215054/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AANSC331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RS 182
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30-DEC-1987;
26-FEB-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-CCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
02-MAR-1990
                                                                        21 - NOV - 1989
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AAP92047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTRTIASPKGPVIQMYINVDKDLVGWPAPQGSRSLTFCTGGSSDLYLVTRHADVIPVRRA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is encoded by the composite CDNA of AAN90327. These antigens react with antibodies in patients with non-A non-B hepatitis (NANBH). They can be used to diagnose HCV-induced NANBH, to raiso antibodies for immunoassay or treatment, or to produce vaccines. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus gene - used for prodn. Of polymolectide probes, polymeptide(s) and antibodies for diagnosis, prevention and treatment of infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gabs
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                                                                                                                                                                                                                                                                                                                                                            Protein sequence of hepatitis c virus composite cONA.
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                                                                    AAP90158 standard: protein: 1786
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87US-0139886.
88US-0161072.
88US-0263584.
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                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; vaccine
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Best Local Similarity 98.45
Matches 179; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-215054/30.
N-PSDB; AAN90327.
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RS 491
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Kuo
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179; Conservative
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                                                     Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAN92106
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RS 757
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                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON
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30-DEC-1987;
26-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                Houghton M,
                                                                                                                                                        18-NOV-1988;
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01-NOV-1989
                                                                                                                                                                                                                                             06-MAY-1988;
                                                                                                                                                                                                                                                             26-0CT-1988;
                                                                                                                                                                                                                                                                             14-NOV-1988;
                                                                                                                      31-MAY-1589
                                                                                      EF318216-A.
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(Updated on 25-MAR-2003 to correct PR ifeld.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRSLTPTTGGSSOLYLVTKHADV1PVRRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDSRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIFVESLETTM 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAPITAYAQQIRGLIGGIIISLIGRDKNOVEGEVOIVSTAACIFLAIGINGVOWIVYHGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                   Repatitis C virus (HCV): non-A. non-B hepatitis (HAMBH).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Purified hepatitis C virus - and associated nucleic acids and polypeptide(s) \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 943; 25 16;
Pred. No. 1.2e-88;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Figure 32-1 - 32-7; 139 pp; English
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                                                                                                                                                                                                                                                                                                                                                                K10 G1
                                                                                                                                                                                                     870S-6122714.
870S-6139986.
880S-0161072.
880S-0191262.
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                                                                                                                                                                         88EP-0310922
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                              Houghton M. Choo Qi.
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1989-159274/22.
                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2301 AA;
                                                                  Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB: AAN92103
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                                                                                                                                                                                                   18-NOV-1987;
30-DEC-1987;
26-FEB-1988;
06-MAY-1988;
26-OCT-1988;
                                                                                                                                                                       18-NOV-1988;
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02-MAR-1990
                                                                                                                                      31-MAY-1989
                                                                                                                                                                                                                                                                                            14-NOV-1988
                                                                                                    EP318216-A.
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ID AAP9
XX AC AAP5
XX DT 25-h
DT 02-h
XX DE Sequ
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It is the sequence encoded in the open reading frame of hepatitis C virus (HCV) cDNA inserts in clones K9-1 through 15e. It is antigenic and could be used in immunoassay reagents and vaccines and to generate antibodies useful in diagnosis and passive immunotherapy for HCV infection/non-A, non-B hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GTRT1ASPKGPVIQMYINVDKDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  indels
Hepatitis C virus (HCV); non-A, non-B hepatitis (HANSH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and associated nucleic acids and polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Figure 47-1 - 47-8; 139 pp; English
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87US-0139686.
88US-0161072.
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61 GIRIIASPKGPVIOMYINVDKDLVGWPAPQGSRSJJTPCTCGSSDLYLVTRHADVIPVRRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a pharmaceutical composition which comprises a hepatitis C virus (HCV) antisense polynucleotide. The HCV is characterized by a positive stranded RNA genome which has allow homology at the polypeptide level to a HCV polyprotein. The antisense polynucleotide binds to cellular polynucleotides which chance and/or are required for viral infectivity, replicative ability, or chronicity. The antisense polynucleotides which designed to bind with high specificity, to be of increased stability, to be stable and to have low toxicity. The composition also comprises a agent which causes viral RNA to be inactive. The composition is used for preventing HCV replication in a system. The present sequence is encoded by a novel HCV cDNA sequence, which is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAPITAYAQQTRGLLGCIITSLTGKDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynuciotide which is complementary to or corresponds to a sense
strand of the virus genome, and selectively hybridises to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.0%; Score 943; DB 21; Length 2772; 98.4%; Pred. No. 1.6e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition comprising a hepatitis C virus antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR34009 standard; Protein; 2816 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example: Fig 16: 75pp: English
                                                                                                                                                                                       89US-0325338.
89US-0341334.
89US-0355002.
90EP-0302865.
                                                                                                                                                                                                                                                                                                                                                                                                               Kuc G;
                                                                                                                             2000EP-0109602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 98.4 ses 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
                                                                                                                                                                                                                                                                                                                                                                                                            Choo C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-566891/53.
                                                                                                                                                                                                                                                                                                                                                     (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2772 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCV-1 polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
1092 RS 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAA75296
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                                                                                                                             16-MAR-1990;
      EP1034785-A2
                                                                                                                                                                                       17-MAR-1989;
20-APR-1989;
                                                                                                                                                                                                                                                                                     .6-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
26-JUL-1993
                                                                                                                                                                                                                                                    8-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                               Houghton M,
                                                                   13-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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         $\circ{\circ}{\circ} \circ{\circ}{\circ} \circ{\circ}{\circ} \circ{\circ}{\circ} \circ{\circ}{\circ} \circ{\circ}{\circ} \circ{\circ}{\circ} \circ \ci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRSLTPCTCGSSDLY;VTRHADVIPVRRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ()
()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAPITAYAQQTRGLLGGLLTSLTGRDKNQVEGEVQIVSTAAGTFLATCINGVCWTVYHSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is the peptide encoded by the composite hepatitis C virus (HCV) cDNA of AAN90336. The polypeptides are used to diagnose HCV-induced NANBH. To raise antibodies for immunoassay or treatment, or to produce vaccines.

(N.B. This record was resubmitted to correct errors in the sequence.) (Updated on 25-MAR-2003 to correct PR [Held.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus gene - used for prodo. of polypucleotide probos,
polypeptide(s) and antibodies for diagnosis, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by a cDNA compiled Hepatitis C virus cDNA clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV, antisense polynucieotide; polyprotein; viral replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.0%; Score 943; DB 10; Length 2436; 98.4%; Pred. No. 1.36-86; iive 3; Mismatches 6; Indels 9
Hepatitis C virus; clone 15e; clone k9-1; probe; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, fig 47-1 to 47-8; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB18540 standard; Protein; 2772 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuo G;
                                                                                                                                                                                                                                                                                                              8705-0122714.
8705-0139886.
8805-0161072.
8605-0263584.
                                                                                                                                                                                                                                                    8868-0027024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORPORATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 98.4 Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheo Qi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1989-215054/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus;
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                                                                   Pan troqicdytes
                                                                                                                                                                                                                                                                                                           18-NCV-1587;
30-DEC-1987;
26-FEB-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghton M,
                                                                                                                                                                                                                                                    18-NOV-1988;
                                                                                                                             GB2212511-A
                                                                                                                                                                                       26-JUL-1989
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AAB18540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the entire hepatitis C virus polyprotein. HCV is a member of the flavivirus family and appears to encode a basic polypeptide domain (°C") at the N-terminal of the virai polyprotein, followed by two giycoprotein domains ("El", "E2/NSI"), upstream of the nonstructural genes N2 through NS5. See also AAQ39134-48, AAR35982-4008 and ARR38088-89.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
HCV, asymptomatic; chronically infected; epitope; viral isolate; domain; immunological; cross-reactive; eavelope protein; vaccine; qp53(BVDV)/qp55; hog cholera virus; pestivirus; NS); flavivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immuno-reactive hepatitis C virus polypeptide compsns. - contg. at least 2 sequences from the first variable domain of distinct HCV isolates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.0%; Score 943; DR 14: 98.4%; Pred. No. 1.60-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composite hepatitis G virus (HC-J1/GDC/CHI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 9; 106pp; English.
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                                                                                                                                                                                                                                                                           9105-0759575
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                                                                                                                                                                                                                                                                                                                                                                      Houghton M, Weiner AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (updated)
                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-117468/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2816 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus.
                                                                                           Repatitis C virus
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                                                                                                                                                                                                                                                                           13-SEP-1991;
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                                                                                                                                    WC9306126-A1
                                                                                                                                                                                  01-APR-1993.
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61 GTRTIASPKGPVICMYTNVDKDLVGWPAPOGSRSJTPCTCGSSDLYLVIRHADVIPVRRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GDSRGSILSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAPITAYAQQTRGLLGCIIISLIGRDKNQVEGEVQIVSTAAQIFLAICINGVCWTVYHGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                       AAR70230 is the composite hepatitis C virus (HC-JI/CDC/CHI) protein from which the synthetic HCV antigens described in AAR70310-R70229 were derived. These synthetic antigens can be used to screen blood, or blood products for the presence HCV, they can also be used in various specific assays for the detection of HCV antibodies, and
                                                                                                                                                                                                                               Synthetic antigens for the detection of hepatitis C virus antibodies - comprise portions of the HCV peptide sequence, for use in screening blood and blood products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus; HCV; J1; J7; HCV-1; non-A, non-B HCV; NANBH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                            Van Heuverswyn H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 943; DB 16;
Pred. No. 1.7e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                             antiqens, or as immunoqens.
("Dpdated on 25-MAR-2003 to correct PN field.)
("Dpdated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "encoded by TI"
Misc-difference 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY14975 standard; Protein: 2955 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                            Pollet D,
                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of HCV-1 ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.0%;
                                                                  90EP-0124241.
                                  94EP-0108611.
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(first entry)
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179; Conservative
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                                                                                                                        INNO-) INNOGENETICS NV
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                                                                                                                                                              Maertens
                                                                                                                                                                                              WPI; 1995-116946/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2894 AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1206 RS 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RS 182
                                                                  14-DEC-1990;
14-DEC-1990;
                                  14-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-2003
08-NOV-1999
22-MAR-1995
                                                                                                                                                            Deleys RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY14975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
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/note- "encoded by CCCC"

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The invention provides two new isolates of hepatitis C virus (HCV). Ji and and J7. Those two isolates comprise nucleotide and arise acid sequences that are distinct from the HCV isolate MCV-1. The nucleotide sequences may be used to detect non-A. HCV (MANH) polynucleotides by hybridisation for diagnosis of NANH infections. They may also be used to screen blood donors, donated blood and blood products for this infection. The isolates may also be used to isolate other naturally occurring variants of the virus. The polypeptides may be used as a vaccine for variants of the virus. The polypeptides may be used as a vaccine for present sequence represents the unite against intection with NANHH. The present sequence represents the unite adding sequence of HCV-1 DFF. (Updated on 20-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GTRITASPKGPVIQMYTNVDKDINGWPAPQGSRSLIPCTCGSSDLYLVTRHADVIPVRRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAPITAYAQQIRGLLCCITTSLTGRDKNQVEGEVQIVSTAAQIFLATCINGVCWTVYHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                    New Hopatitis C Virus isolates, useful for disensels of hepatitis infections and development of vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.0%; Score 943; DB 20; Length 2955: 98.4%; Pred. No. 1.7e-88;
Live 3; Mismatches 0; Indels 0.
                                                                                                                                                                                                                         on M. Irvine BD, Kolberg JA:
Weiner AJ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: September 27, 2003, 12:16:53 Job time: 79 secs
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                                                                                                                     8908-0408045.
8908-0456142.
90EP-0310149.
                                                                                                                                                                                                                              J, Houghton M,
Saite I, Weine
                                                                                          99EP-0101746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 98.40
Watches 179, Conservative
                                                                                                                                                                                                                                                                          WPI: 1999-480843/41.
                                                                                                                                                                                  (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2955 AA;
                                                                                                                                                                                                                                                                                         N-PSDB; AA207656
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                                                                                                                                                                                                                              Han J,
                                                                                                                                                                                                (CYAA/) OYA A.
                                                                                                                                        21-DEC-1989;
17-SEP-1990;
                                                                                                                                                                                                                                             Miyamura T.
                                                                                         17-SEP-1990;
                                                                                                                      15-SEP-1989;
                               EP939128-A2.
                                                             01-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1085
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September 29, 2003, 18:58:12; Search time 32 Seconds (without alignments) 44.642 Million cell updates/sec
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| SIDSI/gcgdala/geneseq/geneseqp-embiAA41982.DAT:
| SIDSI/gcgdala/geneseq/geneseqp-embiAA1984.DAT:
| SIDSI/gcgdala/geneseq/geneseqp-embiAA1985.DAT:
| SIDSI/gcgdala/geneseq/geneseqp-embiAA1985.DAT:
| SIDSI/gcgdala/geneseq/geneseqp-embiAA1986.DAT:
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| SIDSI/gcgdala/geneseq/geneseqp-embiAA1986.DAT:
| SIDSI/gcgdala/geneseqp-embiAA1986.DAT:
| SIDSI/gcgdalaA1986.DAT:
| SIDSI/gcgdalaA198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATE
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compuger Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 96%
Listing first 45 summerres

    protein search, using sw model

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44
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 2030000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                     OM protein
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                                                                                                                                                                                                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		φp				
Result No.	Score	Ouery Match	Ouery Match Length DB	DB	CI	Dosertp: Jon
		97 7			250053417	
٠,				1	7750000	1313012012012
7	42	95.5		3.	AAR50072	NANSH virus antige
٣	42	95.5		5.	AAR54066	Nec-A, nec-B hepar
4	42	95.5		9.	AAR98361	SWINEYERSON MILLS
5	7	93.2	3010	20	AAW98022	Infections penalty
9	4	93.2		22	AAB31170	Amino acid segrence
7	17	93.2		7.7	AAB59174	Protein encoded by
8	40	6.06		21		Hopatitis C virus
σ	0.1	90.9		20		HCV NG3 Dro.e.

Human hepatitis C	Encoded by full-le	HCV NS2-NS4 peptid	HCV NS4A-NS3 compl	HCV NS4A-NS3 compl	~	NS4A-NS3	NS4A-NS3	NS4A-NS3	m	A-NS3	NS4A-NS3	ŝ	NS4A-NS3	NS4A-NS3	HCV NS4A-NS3 compl	Mouse T2R05 amino	Composite HCV HC-J	Human secreted pro	Arabidopsis thalia	Arabidopsis thalia	Rabbit EST encoded	Human polypeptide	Bifidobacterium lo	Human ORFX protein	Group B Streptococ	Streptococcus poly	Streptococcus poly	dopsis	Novel human diagno	isiae	רס	liagn	5	1.13	Human albumin fusi
AAR34580	AAR34468	AAR29854	AAY17888	AAY17890	AAY:7879	AAY17882	AAY 1788 3	AAY17886	AAY 17878	AAY24950	AAY24941	AAY24942	AAY24945	AAY24946	AAY17891	AAB87759	AAR24440	AAB34473	AAG19987	AAG4 C288	AAM23525	ABP69510	ABP65529	ABP10525	AAU03665	ABP27696	ABP27695	AAG29992	ABG21362	AAG70686	AHG27847	ABG25216	ABG54761	ABG64762	ABG64945
	74																																		
3010	3011	174	213	215	216	216	216	216	2:5	646	665	665	999	665	667	300	2894	76	354	354	473	473	876	144	18.	339	346	345	908	946	1085	1097	82	82	8.5
88.6	88.6	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84	84	84.3	34.1	34.1					79.5										77.3			75.0		
39	on m	37	37	37	3.7	37	3.7	3.7	37	37	3.7	3.7	37	3.7	37	36	36	35	35	35	35	35	35	34	3.4	3.4	÷	₹.	₹. *\	m T	~		æ		
10	1,	12	13	1.4	15	16	17	18	19	20	2.1	7.7	23	24	2.5	9.7	2.7	(Z)	6.7	(*) (*)		. C.	en e.	₹†:	u:	ď.	5.6	un:	\$\frac{1}{2}\text{*}	S <b>P</b>		42	43	77	4.5

## ALIGNMENTS

RESULT 1

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Polymerase chain reaction, PCR, amplify, primer: non-A, non-B hepatitis;
NANBH; virus; blood transmissible; detection; hepatitis virus; RT-PCR;
C100 annibody; HCV RNA; NS5 region.
                                                                                                                                                                                                                                                                             /label- Ser, Arg, Gly
Misc-difference 400
        AAR53417 standard, Protein, 3010 AA.
                                                                                                                                             Location/Qualitiers
                                                                 Blood transmissible NANBEV protein.
                                                                                                                                                                                                                                                          /label= Gly, Asp
Misc-difference 398
                                                                                                                                                               /label- Bis, Arg
                                                                                                                                                                                                                            Asn
                                                                                                                                                                                                                                               Ser
                                                                                                                          Non-A, non-B hepatitis virus.
                                                                                                                                                                                    /label= Cys,
                                                                                                                                                                                                       /label- Leu,
                                                                                                                                                                                                                          /label- Asp,
                                                                                                                                                                                                                                               /label- Phe,
                                              (first entry)
                                                                                                                                              Key
Misc-difference 222
                                                                                                                                                                           Misc-difference 225
                                                                                                                                                                                              Miss-difference 246
                                                                                                                                                                                                                                                        Misc difference 311
                                                                                                                                                                                                                                    Misc-difference 293
                                                                                                                                                                                                                 Misc-difference
                                              17-JAN-1995
                          AAR53417;
AAR53417
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Len

Asp

Phe,

Val

Asp

label- Gln, Pro, label- Lys, Arg /label= Scr, Asn label= Thr, Ala label= Gly, Tle /label- Cys, Arg /label= Val. Met label- i.eu, Met Tabel- Cys, Arg /iabel- Tyr, Cys label Thi, Ala /label= Leu, 1017 /label= Leu, 2917 label= Met, /label= Asn, 1828 label Lys. label Asn, label= Met, label 3ly, label- Arg, label- Arg, 'label+ Glu, label- Asn, label- Gly, label- Ala, label- Clu, label- Asp. /label- Ser, 92JP-0051885 92JP-0051885 labelabel 2488 Misc-difference 1455 Misc-difference 2968 WPI; 1994-163130/20. N-PSDB; AAQ63499. Misc-difference 2865 Misc-difference 410 (KAEN/) KAENNO K. Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difierence Misc-difference JP05105690-A 10-MAR-1992; 10-MAR-1992; 19-APR-1994 

Va L :: 5 G

Asp

Asp

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This sequence is encoded by the genome of a blood transmissible non-A, non-B hepatilis (NAMBE) virus. The cDNA sequence was isolated using the primers given in AAG63500-35. The amplified fragments are used in the detection of hepatilis virus. The target DNA was isolated from serum of chronically infected NAMBH patients who were C100 antibody-positive and HCV RNA (NS5 region) positive. Reverse transcription-PCR and PCR were performed on cDNA and the total human NAMBH DNA was constructed from 23 clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the sequences given in AAR50068 and AAR50070-82 represent antigens of structural and non-structural regions of non A non B hepatitis virus (NANBHY). The CDNA encoding these sequences wase derived from the plasma of a NANBH patient by recombinant DNA techniques. These fragments are useful for the diagnosis of NANBH patients and the detection of NANBHY carriers.
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen: structural, non-structural: non A non B hepatitis virus;
NANBHV: NANBH; patient: plasma; diagnosis; detection; carrier: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid fragment coding non-A non-B hepatitis virus antigen - useful in diagnosis of NANB patient and detection of virus
                                                                                                                                                                                                                                                                   ö
rosed for
                                                                                                                                                                                                                                    DB 15: Length 3010;
65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 273;
                                                                                                                                                                                                                                                                   Indels
Blood transmissible non-A non-B hepatitis virus DNA
                                                                                                                                                                                                                                                                   ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 15;
Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TOKR-) 2H TOKYOTO RINSHO IGAKU SOGO KENKYUSHO
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                    Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 18-19; 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                           Clain 1: Page 8-20; 22pp: Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SANWA KAGAKU KENKYUSHO CO. TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NANBH virus antigenic fragment #4
                                                                                                                                                                                                                                                                                                                                                                                                  AAR50072 standard; Protein; 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.5%;
                                                                                                                                                                                                                                    97.78;
88.98;
             detection of hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non A Non B hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93JP-0156087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92JP-0207391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                       1039 LIGCIVISL 1047
                                                                                                                                                                                                                                                                                             1 LIGCIITSL 9
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                                                                                                                                                                                                        301C AA;
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Best Local Similarity
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUE-1992;
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                                                                                                                                                                                                           Sednerge
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                                                                                                                                                                                                                                     Query Match
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The sequences given in AAR98361-62 response the 5'UTR/CCRE/ENV/NS1/NS2/NS3 protein region derived from hepatitis C virus (HCV) isolates #4 and #6 respectively. The proteins partic, contain amino acids 384-495 of the HCV NSI antiquen. These protein fragments may be used in the detection of antibodies against HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant polypeptide comprising partial NSI region of hepatitis
non-A non-B viral antigen - used in a method for detecting
antibodies against hepatitis non-A non-B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCV, infectious clone; infection; diagnosis; therapy; vaccine;
screening; assay; antiviral; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Infectious hepatitis C virus genotype 1b strain HC-J4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.5%; Score 42; DB 16; Length 1051; Best Local Similarity 88.9%; Pred. No. 35; Matches 8; Conservative 1; Mismatches 0; Indels (
                                                                         Hepatitis C virus; HCV; antigen; detection; antibody.
                                             5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 10-12; 15pp; Japanese.
                                                                                                                                                         Core peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW98022 standard; Protein; 3010 AA.
                                                                                                                             Location/Qualifiers
1..191
/label Core peptide
                                                                                                                                                                                                              /label- NSi/NS2
811..1051
/label- NS2 and NS3
                                                                                                                                                                    192.383
/label- ENVI
384.810
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                 22-AUG-1996 (first entry)
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1039 LIGCIITSL :047
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N-PSDB; AAT30386.
                                                                                                                                                                                                                                                                                                                                                                                      (TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1051 AA;
                                                                                                  Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09904008-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - useful for
                                                                                                                                                                                                                                        , non-B hopatitis virus; NANBHV; hepatitis C virus; ECV; ENV; NS1; NS2; NS3; antiden; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 15; Length 1051;
Pred. No. 35;
  Inde.s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA coding a Non-A, non-B hepatitis virus antigen detecting HCV within serum
 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANW ) SANWA KAGAKU KENKYUSHO CC.
(TOFU ) IONEN CORP.
(TOKR-) ZH TOKYOIO RINSHO IGAKU SOGO KENKYUSHO
                                                                                                                                                                                                              Non-A, non-B hepatitis virus gene #4 product.
Mismatches
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/label= NS2-NS3
/note= "NS3 N-terminal"
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                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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86.9%;
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/label= core
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                                                                                                                                                                                                                                                                                                                                                                    /label- ENV
384..810
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 Conservative
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                                            1 LLGC(ITSL 9
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                                                                                                                                                                                                                                                                                 Hepatitis C virus.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AABS9174 standard; Protein; 3010 AA.
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88.9%;
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Rest Local Similarity 88.5
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                                                                                                         WPI; 2001-071081/08.
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                                                                                                                                                                                                                                             signs and symptoms
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                                                                                                                             N-PSDB: AAC86939.
                                                                Nam J, Bukh J.
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AAB59174
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BCV; vaccine: viral inhibitor: antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infectious nucleic acid sequences can also
                                                                                                                                                                                                                                                                                                                                                                                                             This protein is encoded by the infectious hepatitis C virus (HCV) genotype ib strain HC-J4 genome (see AAX2483). [G.-J4 was obtained from acute phase plasma of a chimparzee infected with serum containing HC-J4/91. The infectious nucleic acid sequence can be used to produce chimeric genomes (see AAX2483) consisting of the open reading frames of infectious nucleic acid sequences of other genotypes (including genotypes 1-6) and subtypes (such as lb. 2a, 2b, 2c, 3a, 4a-f, 5a and 6a) of HCV. The invention also relates to the introduction of mutations or deletions into infectious nucleic acid sequences in order to produce an attenuated HCV virus suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be used to produce attenuated virus via passage in vitro or in vivo of the viruses produced by transfection of a host ceil with the infectious nucleic acid sequence. Vaccines comprising one or more polypeptides made from the infectious nucleic acid sequence are used to immunise mammals, especially humans, against hepatitis C. The nucleic acid sequences can also be used to induce protective immunity against the virus. The nucleic acid sequences or their encoded proteases (e.g. NR3 protease) can additionally be used to develop screening assays to identify antiviral agents for HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a hepatitis G virus (HCV) clone genetype (b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G
                                                                                                                                                                                                                                                                                  New isolated hepatitis C virus mudleic acids - used to develop products for the diagnosis, preventiom and treatment of MCV infections and for developing screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41: 58 Zer Lenath 3013;
Prod. No. 1.58-62;
1; Mismatches 6: Indels ...
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                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                           Purcell RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.2%;
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                      98WD-US14688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for vaccine development.
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les 8; Conserv
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                      :6-JUL-1998;
                                                                27-JAN-1998;
                                                                                      18-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as antiviral agents. Formulations or compositions comprising the chimeric virions may be used to treat or prevent the signs and symptoms of HCV. The present sequence is encoded by a HCV clone, which is used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                         New nucleic acid comprising a chimeric bovine viral diarrhoea virus genome in which the (non-)structural region has been replaced by hepatitis C virus (HCV) genome useful for treating or preventing HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by infectious Repatitis C virus 1b genetype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to construct chimeric nucleic acids of the invention
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Emerson SU, Purcell RH;
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the fusion polypeptide.
                        184 AA;
                                                                                                                                                                                                                               11-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1999.
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                        Sequence
                                                                                                                                                                                                       AAW93482;
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ID AAR3
                                                                                                                                                          SESTILI 9
                                                                                                                                                                        AAK93482
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SS X SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present protein sequence is the catalytic domain of the NS3 clone from the 1B genotype, derived from hepatitis C virus, The NS3 protein has a sequence relationship to members of the trypsin family of serine proteases. Constructs comprising an NS4 peptide requence covalently attached to the N-terminus of NS3 catalytic domain or their fragments and be used to create fusion polypeptides. This fusion polypeptide contains the NS3 domain expressed in a size, soluble form. This facilitates the use of the polypeptide in direct screen.ng of potential anti-viral compounds, that are used for diagnosts and treatment of hepatitis C virus infection. It is also used to seroen for inhibitors of serine protease activity. The polymucicotides are also useful to identify diagnostic or therapeutic compounds and for recombinant production of
                                                                                                                                                                                                                                                                                                                                                              NS3 catalytic domain: NS4A peptide: NS4A-NS2 fusion construct: diagnosis: serine protease; trypsin family; screening: anti-viral compound: treatment: inhibitor; therapeutic.
                                     The present invention relates to GB virus-B. The nucleic acid molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /oote= "Residues that are deleted for the construction of NS4A/NS3 fusion construct"
                                                                                                                                                          Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptide comprising hepatitis C virus NS4A and NS3 domains, useful for screening for compounds useful for the diagnosis and treatment of hepatitis C virus
                                             of the invention are useful for indirectly studying the molecular properties of hepatitis C virus (670). The infectious nucleic acid sequence of the GB virus-A clone and the HCV/33V-H chimeras may be in the development of vaccines and therapeuties for HCV.
                                                                                                                                                          ä
                                                                                                                                  Length 3010;
                                                                                                                                                          0; ::dels
                                                                                                                                                                                                                                                                                                                                           Repatitis C virus NS3 datalytic domain of 1B genotype.
                                                                                                                                  Score 41; DB 22:
Pred. No. 1.5e+02:
                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..5
                                                                                                                                                                                                                                                                   AAY44727 standard; Protein; 184 AA
          Disclosure, Fig 7; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Fig 1; 30pp; English.
                                                                                                                                  93.2%;
88.9%;
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                                                                                                                                                                                                                                                                                                                   04-MAY-2000 (first entry)
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                                                                                                                                                          Conservative
                                                                                                                                                                                               1 LIGCIITSL 9
                                                                                                                     Query Match
Best Local Similarity
From 8, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYFL ) UNIV FLORIDA
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                                                                                                           3010 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                   Repatitis C virus.
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                                                                                                           Sequence
                                                                                                                                                                                                                                                                                         AAY44727
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New hepatitis C virus NS3 helicase crystals - which provide molecular design techniques to identify, select and design agents which bind to the helicase, particularly inhibitor compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NS3; helicase domain; X-ray crystal structure; Hepatitis C virus; HCV; computer programme; bluding pocket; three-dimensional.
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                         Length 184;
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                       ore 40; DB 2
red. No. 15;
Mismatches
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                         Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR34580 standard; Protein; 3010 AA.
                                                                                                                                                                                                                                                                     AAW93482 standard; Protein; 631 AA
      90.9%; Sco.
300.0%; Pre
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                                                                   Conservative
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                                                                                                             Cuery Match
Best Local Similarity
8; Conserve
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Matches 8: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                     ECV NS3 protein
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The sequences given in AAR29852-70 are encodeed by various clones which
                                                                                                                                                                                                                            CONA was prepared from HCV genomic RNA. Full-length close JK1-5 and 14 shorter closes were isolated by PCR amplification.
Primor/probes derived from the sequences of these clones can be used in diagnostic assays for HCV. See also AAQ40425-C40439.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone: polypeptide; NS2-NS4: Hepatitis C: Virus; HCV; serum; HC; transcriptase; cDNA; primer; allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections
                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                   Score 39; DB 14; Length 3Cli;
Pred. No. 3.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                  DNA and cDNA of hepatitis C virus – useful as probes for diagnosing HCV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 151-52; 305pp; English
                                                                                                                                                                                                Claim 3; Page 6-18; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR29854 standard; Protein; 174 AA.
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                                                                           (SANW ) SANWA KAGAKU KENKYUSHO CO
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91JP-0172794.
91JP-0287008.
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92JP-0099957.
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                 91JP-0153736
                                              91JP-0153736
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(first entry)
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Best Local Similarity 7/.v.
                                                                                                                                                                                                                                                                                                                                                                                                                              1039 LFGCIVTSL 1047
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                                                                                                                                                                                                                                                                                                                                                                                                 1 LLGCIITSL 9
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N-PSDB; AAQ32485.
                                                                                                          WP:; 1993-130638/16.
                                                                                                                                                                                                                                                                                                         3011 AA;
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                                                                                                                          N-PSDB; AAQ40426
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12-JUN-1991;
67-OCT-1991;
                 30-MAY-1991;
                                              30-MAY-1991;
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20-APR-1992;
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                                                                                                                                                                                                                                                                                                           Sednence
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AAR29854
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                                                                                                                                                                                                                                                                                                                                                                                                Single or double stranged deoxyribonucleic acid for heparitis C vizebetction - comprises 9500 nocleotide(s) and encodes fuman hepatitis C virus gene, for diagnosis by polymerase chain reacting serum sample RNA deriv, and electrophoresis
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                                                                                                                                                                                                                                                                                                                         Suzaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.6%; Score 39; Da 14; Honath 3010; 72.8%; Pred. No. 3.4e-02; tive 1; Mismatches 1; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV; non-A, non-B hepatitis virus; NANXHV; liver disease; polymerase chain reaction; diagnostic method.
                                                                                                                                                                                                                                                                                                                         Sawa: K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Encoded by full-length Hepatitis C virus close UKI 5.
                                                                           Human hepatitis C virus gene encoded polypoptide
                                                                                                                                                                                                                                                                                                                         Kurcho M. Mitani I,
                                                                                                          HCV; detection; diagnosis; vaccine; peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 4-20; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "not defined"
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2414
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(first entry)
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                                                                                                                                       Human hepatitis C virus.
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                                25-MAR-2003
                                                25-AUG-1993
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AAR34580;
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Gaps

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0; Mismatches

DB 26; Length 213; 60; i; Indels

Score 37; Pred. No.

84.18; 88.9%;

Guery Match
Esst Local Similarity 88.9
Matches 8; Conservative

47 LLGCKITSL 55

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Were used in the isolation of the NS2-NS4 regions of the Hepatitis C Virus (HCV) dene of the invention (see also AAR29660, AAR29559-60 and AAR29843-51). These NN sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into CDNA using transcriptase in the presence of one amplification from the serum of a AAR2576-79. The sequences were then amplified using primer pairs. The CDNA sequences isolated represent different alleles of the same region of the HCV dene. Sequence comparisons of these cromes showed that it is possible for a patient to carry more than one HCV strain at one time. See also AAR32436. (Updated on 25-MAR-2503 to correct PN field.)
                                                                                                                                                                                                                                                                                       or Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV: hepatitis C virus: single chain recombinant complex: linker:
NS3 protease; NS4A cofactor; NS4A-NS3 complex; serine protease;
hydrophobic domain; covalent complex; detection: inhibitor.
                                                                                                                                                                                                                                      DB 139 December 1749
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Pred. No. 45;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example it Page 119; 211pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weber PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY17886 standard, Protein: 213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV NS4A-NS3 complex SEQ 1D NO:50.
                                                                                                                                                                                                                                                   84.1.48
98.98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                       56 LLGCNITSL 64
                                                                                                                                                                                                                                                                                                                      1 ELECTITSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI: 1999-385385/32.
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                  174 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9928482-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 - NOV - 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Malcoim BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY17888;
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
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covalent protease-peptide complexes previously available.

213 AA

Seguence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a covalent hepatitis C virus (MCV) NS4A-NS3 complex comprising a central hydrophobic domain of native HCV NS4A-NS3 complex. Infact, and an HCV NS3 serine protease domain, where the hydrophobic domain of native HCV NS4A peptide is tethered by the linker to the amino terminus of the HCV NS4A peptide is tethered by the linker to the amino terminus of the HCV NS3 protease domain. The present sequence represents an example of the above complex. The covalent NS4A-NS3 complexes are useful for structural determination and determination of mode of binding of HCV inhibitors by NMR spectroscopy. They can also be used for detecting inhibitors of the protease activity, the helicase activity and the Alpase activity of NS3. The covalent covalent protease premide complexes previously available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                         HCV: hepatitis C virus; single chain recombinant complex; linker; NS3 protease; NS4A cofactor; NS4A-NS3 complex; serine protease; hydrophobic domain; covalent complex; detection; inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.18; Score 37; DB 20; Length 215; 88.9%; Pred. No. 60; Live 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hepatitis C virus covalent complexes
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Weber PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY17879 standard; Protein; 216 AA.
              AAY17890 standard: Frotein; 215 AA.
                                                                                                           HCV NS4A-NS3 complex SEQ ID NC:57.
                                                                                                                                                                                                                                                                                                                                               98US-6694331.
97US-6067315.
                                                                                                                                                                                                                                                                                                                   98WC-US24528
                                                                             07-SEP-1999 (first entry)
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 (SCHE ) SCHERING CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              API; 1999-385385/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 AA:
                                                                                                                                                                                                      Reparitis C virus
                                                                                                                                                                                                                                                    W09928482-A2
                                                                                                                                                                                                                                                                                                                   24-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                   38-JJL-1888;
                                                                                                                                                                                                                                                                                                                                                                  28-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Malcolm BA,
                                                                                                                                                                                                                                                                                    9661-NC2-01
                                                                                                                                                                                                                        Synthetic.
                                              AAY17890:
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ID AAY
AAY17890
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The present invention describes a covalent hepatitis C virus (HCV) NS4A-NS3 complex comprising a central hydrophobic domain of native HCV NS4 serine protease domain, where the hydrophobic domain of native HCV NS3 serine protease domain, where the hydrophobic domain of native HCV NS4 protease uchain. The present to the amino terminus of the HCV NS4 protease uchain. The present complex. The covalent NS4A-NS3 complexes are useful for structural determination and determination of mode or Ending of HCV intibitors by NMR spectroscopy. They can also be used for detecting inhibitors of the protease activity, the holicase activity and the ATPASE activity of NS3. The covalent NS4A-NS3 complexes are mode activity and active are also be used for detecting inhibitors of the protease activity and the ATPASE activity of NS3. The covalent proteases activity and the atPase activity the file the non-covalent protease-poptide complexes previously available.
                                                                                                                    ECV: hepatitis C virus: single chair recombinant complex: lister:
NS3 protease; NS4a colactor: NS4a-NS3 complex: serine protease;
hydrophobic domain; covalent complex: detretion: inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 37: DB 20; Legath 216:
Pred. No. 61:
0: Mismatches 1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New hepatitis C virus covalent complexes
                                                                                                                                                                                                                                                                                                                                                                                                                                           Weber PC, Yao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6: Page 75-76: 211pp: English.
                                                                                       HCV NS4A-NS3 complex SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.18;
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97US-0067315.
                                                      (first entry)
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Best Local Similarity 88.9
Matches 8: Conservative
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                                                                                                                                                                                            Hepatitis C virus.
Synthetic.
                                                                                                                                                                                                                                               W09928482-A2
                                                                                                                                                                                                                                                                                                                  24-NOV-1998;
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                                                    07-SEF-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Malcolm BA,
                  AAY17879;
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September 29, 2003, 19:07:23

Search completed: Job time: 35 secs

11'.! 11. LLGC:KTSL 56 1 LLGCLITSL 9

9. P

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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using sw model - protein search, OM protein

September 29, 2003, 19:03:22; Search time 18 Seconds (without alignments) 48.084 Million cell updates/sec Run on:

US-09-965-594-1\_COPY\_14\_22 44 Title: Perfect score: Sequence:

1 LLGCIIISL 9

BLOSUM62 Gapop 10.0 , Gapext, 0.5 Scoring table:

96168682 residues 283308 seqs, Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Disting tirst 45 summaries Post-processing: Minimum Match 99% Maximum Match 99%

p[:1]:\* pir2:\* pir3:\* pir4:\* PIR\_76:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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19	33	ĽΛ			734544	hypothetical prote
20	33	S)	•	7	102930	lysine-ketoglutara
21	<b>*</b>	S.			PFHUGA	planelet-derived g
22	32	$\sim$			H90459	hypothetical prote
23	32	$\sim$		•	AG0459	Sec-independent pr
24	32	$\sim$			512864	retinal isomerase
25	32	72.7			C89045	protein B0238.6 [1
26	32	$\sim$			069648	~
27	32	2	348		C83994	aldose l'epimerase
28	32	72.7	367	.7	C82943	e AB
	32	72.7	393	Ŋ	D65238	hypothetica, 44.4

genome polyprotein - hepatitis C virus (strain Taiwan) N:Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonst protein NS4a; nonstructural protein NS4b; nonstructural protein NS5 C:Species: hepatitis C virus

1039

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GNWVIN

A:Note: host Homo sabiens (man) C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 19-Jan-2001 C:Accession: A40244

postsynaptic membr	acetyi-CoA C-acety	probable acyl-CoA	alpha galactosidas	probable glucomate	putative helicase	protein-glutamine	hypothetical prote	hexose transport p	hecose transporter	protein F2H15.10 [	hypothetical prote	protein-glutamine	Sec76 domain prote	saccharopine dehyd	semaphorin F precu
A60083	AB2984	E98299	JC4522	AD0481	D90122	PD0001	T45955	T43533	T40480	H86313	T13460	A29996	T38419	T05195	CC5928
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	a	25	3.2	32	32	32	32	32	3.2	32	32	32	32	32	32
32	č														

## ALIGNMENTS

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C.Acression: A45573
R.Tanaka, T.; Kato, N.; Nakagawa, M.; Ootsuyama, Y.; Cho, M.J.; Nakazawa, T.; Bijib Virus Res, 23, 39-23, 1992
Affile: Molecular cloning of bepatitis C virus genome from a single Japanese carri A:Reterence number: A45573; MUID:92295714; PMID:1318627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Molecule type: DNA
A:Molecul
genome polyprotoin - hepatitis C virus (strain JT)
Nicoludins: capsid protein C: envelope protein M: hepacivirin (BC 3.4.21.98) (nonst
protein NS4a, nonstructural protein NS4b; monstructural protein NS5
protein NS4a; hepatitis C virus
C;bnic: 19-May-2000 *sequence_revision 19-May-2000 *text_change 19-Jan-2001
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Pred. No. 11;
1: Mismatches 0; Indels
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Best Local Similarity 88.9%;
Matches 8; Conservative
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          F;1316-1319/Reqion:
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A; Variety: isolate JK1
D. Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 23-Mar-2001
C; Accession: 518030; 533570; A48332; 518529
R; Honda, M.; Kaneko, S.; Masashi, G.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September: 199:
A; Description: A whole genome of hepatitis C virus chwa was isolated from a single patic A; Accession: 518036
                                                                                                                                                                                                                                                                                                                      Across references: GB: M84754
C; Superfamily: hepatitis C virus denome polyprotein
C; Superfamily: hepatitis C virus denome polyprotein
C; Superfamily: hepatitis C virus denome polyprotein
C; Superfamily: hepatitis C virus
C; Superfamily: hepat
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A.Note: the authors translated the coden AGG for residue 43 as Pro, ING for residue 320 as ITA and TLC for residue 771 as Ser

A.Note: sequence extracted from NCBI backbone (NCRINIL21747, NCBIP:121748)

G.Superfaminy: hepatilis C virus genome polyprotein

Fi.115/Product: capsid protein C #status predicted <NFE>

Fi.16-191/Product: envelope protein F status predicted <NFE>

Fi.30-7006/Product: major envelope protein F status predicted <NSI>

Fi.30-7006/Product: nonstructural protein NSI #status predicted <NSI>
Fi.1007-1615/Product: nonstructural protein NSI #status predicted <NSI>
Fi.11270-1317/Region: nucleotide-binding motif B (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Molecule type: genomic RNA
A:Residues: 1-3010 (40NY)
A:Cross-references: BMBL:X51596: NID:g59478: PIGN:CAA4773.1; PID:g59479
A:Cross-references: BMBL:X51596: NID:g59478: PIGN:CAA4773.1; PID:g59479
A:Experimental source: Isodate UKI from an individial
R:Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakart, S.
Arch. Virol. 128. 163-169, 1993
Arctile: Sequence analysis of purative structural revious of hepatilis C virus isolated
A:Reference number: A48332; MJID:93119270; PKID:8380A22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fil616-1862/Product: nonstructural protein NS4a Fstatus predicted <N4A>
Fil635-2013/Product: nonstructural protein NS4b Fstatus predicted <N4B>
Fi2014-3010/Product: nonstructural protein NS5 Fstatus predicted <NS5>
Fi196,209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207
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1a; nonstructural protein NS4b; nonstructural protein NS5
Richen, P.J.; Lin, M.H.; Tai, K.F.; Liu, P.G.; Lin, G.J.; Chen, D.S.
Virology 188, 152-113, 1992
Wittle: The Taiwanesc hoperitis C virus genome; sequence determination and mapping the
A;Reference number: A40244, MCID:92230206; PMID:1314443
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A;Residues: 1-547,'T',549-621.'V',623-624,'S',626-552,'UL',655-761,'T',763-782 <HGW>
A;Cross-references: EMBL:X61591
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Pred. No. 40;
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88.9%;
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Matches 8, Conservative
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A;Residues: 1-3010 <CHE>
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"Species: Arabidopsis thallana (mouse-ear cress)
A.Variety: Columbia trallana (mouse-ear cress)
A.Variety: Columbia trallana (mouse-ear cress)
A.Variety: Columbia
B.C. Co
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A,Cross-references: EMBL:U28409; NID:g849230; PID:q849234; PIDN:AAC46592.1; CESP:T2:
A,Experimental source: strain Bristol N2
C,Sanetics:
A,Gene: CESP:T25010.2
A,Introns: 35/3; 56/1; 51/3: 76/1; 111/3; 171/1; 201/1
F.1616-1862/Product: nonstructural protein NS4a #status predicted <NV4>
F:1868-3203/Product: nonstructural protein NS4b #status predicted <NV4B>
F:2014-3010/Product: nonstructural protein NS5 #status predicted <NNS>
F:2014-3210/Product: nonstructural protein NS5 #status predicted <NNS>
F:196,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16938
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Pred. No. 61;
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50;
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A;Molecule type: DNA
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Pred. No.
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procession: F508.39 [Imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 (CACCESSION: G86372 (CACCESSION: GACCESSION: G86372 (CACCESSION: GACCESSION: GACCESSION
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Nature 409, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K.C.A.; L.; J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Mar. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ta. A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ta. A.Ritle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MCID:21016719; PMID:11130712
                                                                        A;Cross-references: GB:BA000019; PIDN:BAB72844.1; PID:g17130232; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0887
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Cispecies: Arabidopsis thaliana (mouse ear cress)
Cibte: 0-Mar-2001 Esequence_revision 02-Mar-2001 #text_change 31-Mar-2001
CiAccession: H86372
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83;
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7
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Pred. No. 49;
1; Mismatches
                                                                                                                                                                                                                                                                                        DB .
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85.7%; Pred. No. 8
                                                                                                                                                                                                                                                                                                          77.38;
85.78;
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Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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|LLGCLIT 54
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A; Residues: 1-345 <STO>
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A; Molecule type: DNA
A; Residues: 1-179 <KUR>
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AsMolecule type: DNA
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AD1917
C. Paperical protein al10887 (imported) - Nostoc sp. (strain PCC 7120)
C. Species: Nostoc sp. PCC 7120
A.Note: Nostoc sp. strain PCC 7120
A.Note: Nostoc sp. strain PCC 7120
A.Note: Nostoc sp. strain PCC 7120
C. Date: 14-Dec-2001 *sequence_revision 14-Dec-2001 *text_change 09-Dec-2002
C. Accession: AD1917
R. Rancko, T.: Nakamura, Y.: Wolk, C.P.: Kuritz, T.: Saksmoto, S.: Matanabe, A.: Iriquchi Nakazaki, N.: Shimpo, S.: Sugimoto, M.: Takazawa, M.: Yamada, M.: Yasuda, M.: Tabata, S. DNA Res. B. 205-213, 2001
A.Title: Complete Genomic Sequence of the Filamontous Nizrogen-fixing Cyanobacterium And A. Reference number: AB1807; MJID:21595285; PMID:11759846
A. Accession: AD1917
A. Status: preliminary
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Cispecies: Sis scrofa domestica (domestic pig)
Rivamashita, H. Ichijo, H. Gimsby, S., Morca, A.; ten Dijke, P.; Miyazono, K.
Rivamashita, H. Ichijo, H. Gimsby, S., Morca, A.; ten Dijke, P.; Miyazono, K.
A. Elol. Chem. 265, 1995-2001, 1994
A. Eference number: A49722 hdtD:94124550; PMID:8294451
A. Accession: A49722
A. Status: preliminary
A. Mockuie type: mRNA
A. Residues: 1-653 «YAM»
                                                                                                                                                                                                                                               Conserved hypothetical protein APC706 - Archaeoglobus fulgidus
Cyspecies: Archaeoglobus
Cyspe
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C;Keywords: homodimer: phosphoprotein; signal transduction: transmombranc
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87.5%; Pred. No. 94;
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Pred, No. 41;
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66.7%;
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nes 7: Conservative
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1!!; :1!;
LigcTLTSL 299
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Best Local Similarity
5, Conserve
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A:Cross-references: SGD:S0000290
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                              A:Map position: 2R
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Gene 170, 9-16, 1996
ArItle: Comparison of the promoter proximal regions of the toxin-co-regulated unp gene
A/Reference number: JC4719; MUID:96200848; PMID:8621096
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NAiternate names hypothetical protein YBROBSS
CSPecies: Saccharomycos cerevision of Section 23 Aug. 1995 *text_change 19-Apr-2002
CSPecies: 03-Aug.1995 *sequence_revision 11-Aug.1995 *text_change 19-Apr-2002
CSAccession: $48255, $45954, $44676
RWannhaupt. G.; Stucka, R.; Ehele, S.; Vetter, D.; Foldmann, H.
Ayast 10, 1363-1381, 1994
Astitle: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A:Reference number: $48255; WJID:95208357; PMID:7907426
                                                                                                                                                                                                                                                                                                                                                            toxin-co-requlated protein chain 1 - Vibrio cholerae (fraament)
C;Species: Vibrio cholerae
C;Date: 10-May-1996 #sequencc_revision 19-Jul-1996 #text_change 17-Nov-2000
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A.Molecule type: DNA
A.Residues: 1.946 <a href="https://www.nbig476645">https://www.nbig476645</a>
A.Cross-references: EMBL:X78993: NID:g476645: PIDN:CAA55593.1: PID:g476646
R.Feldmann, H.: Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
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C:Comment: This is a methyl-accepting chemotaxis protein.
C:Genetics:
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85;
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Pred. No. le+02;
0; Mismatches 3
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submitted to the EMBL Data Library, January 1992
                                                                                                                     Pred. No. 85;
                                                                                                   Score 34;
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                                                                                                77.3%;
85.7%;
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A;Molecule type: DNA
A;Residues: 1-401,'RFPKN' <MAN>
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A,Residues: 1-428 <GGI>
A,Cross-references: EMBL:X64098
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                                           Query Match
Best Local Similarity 85.7
Matches 6: Conservative
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A;Accession: S23261
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A;Accession: $45954
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                    A;Gene: F508.39
A;Map position: 1
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A;Gene: SGD:IST2
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C; Genetics:
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A:Cross-references: EMBL:X07743; NID:q35517; PIDN:CAA30564.1; FID:g35518
5:Tyers, M.: Haslam, R.J.: Rachubinski, R.A.; Harley, C.B.
7: Ccll. Biochem, 40, 133-145, 1980
A:Tfile: Molecular analysis of pieckstrin: the major protein kinase C substrate of parkeference number: A45762; MUID:89359547; PMID:2768345
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Clate: 11-Dec 1988 #text_change 20-Apr-2006
Clate: 11-Dec 1988 #sequence_revision 31-Dec 1988 #text_change 20-Apr-2006
Clates: 31-Dec 1988 #sequence_revision 31-Dec 1988 #text_change 20-Apr-2006
Slivers, M.; Rachubinski, R.A.; Stewart, M.I.; Varrichio, A.M.; Shorr, R.G.L.; Hash.
Nature 333, 470-473, 1988
A.Tille: Molecular cloning and expression of the major protein kinase C substrate of A.Reference number: S00755; MUID:88232910; PMID:2887630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Panulirus argus
C.Date: 19-May-2000 *seguence_revision 19-May-2000 *text_change 19-May-2000
C.Accession: 731431
K.Munger, S.D.: Ache, B.W.: Greenberg, R.M.
Submitted to the EMBL Data Library, March 1998
A.Description: Plasma membrane localization of an olfactory inositol 1,4,5-trisphos
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A,Residues: 1-2783 <MUN>
A,Cross-references: EMBL.AP055079; NID:93660666; PID:93660667; PIDN:AAC61691.1
C,Superfamily: inositol-trisphosphate receptor
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N/Alternate names: p47; platelet/leukocyte C kinase substrate (pleckstrin)
C.Superfamily: Saccharomyces cerevisiae probable mombrane protein VBR086c (Superfamily: Saccharomyces cerevisiae probable mombrane protein Keywords: transmembrane protein P:131-:47.7Comain: transmembrane status predicted <TM2> F:156-774.7Comain: transmembrane status predicted <TM3> F:267-24.7Comain: transmembrane status predicted <TM4> F:248-274.7Comain: transmembrane status predicted <TM5> F:506-532.7Comain: transmembrane status predicted <TM5> F:506-532.7Comain: transmembrane status predicted <TM6> F:506-532.7Comain: transmembrane status predicted <TM6> F:566-532.7Comain: transmembrane status predicted <TM6> F:567-588.7Comain: transmemb
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Fred. No. 4.8e+02;
1; Mismatches 1; Inde's
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62.5%;
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2554 LLMCIVTSL 2562
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A; Accession: T31431
A; Status: preliminary
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520 ILGCVITA 527
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Matches 5, Conserv
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A: Residues: 1-350 <TYE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Molecule type: mRNA
A:Residues: 1-350 <TY2>
```

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RESULT 15
D83311
conserved hypothetical protein FA2662 [imported] - Pseudomonas detuginosa (strain FAG1)
C; Species: Pseudomonas aerudinosa
C; Date: 15. Sep. 2006 # Sequence_revision 15. Sep. 2000 # text_change 31. Dec. 2000
C; Accession: D83311
R; Stover, C.K.: Pham, X.Q.: Erwin, A.L.: Mizoquchi, S.D.: Warrenet, P.: Hickey, M.J.: Bit
adman, S.: Yuan, Y.: Brody, L.L.; Coulter, S.N.: Folgor, K.R.: Kas, A.: Larbig, K.: Lim,
Jory, S.: Oison, M.V.
Nature 406, 959-964, 2000
A; Titlo: Complete genome sequence of Pseudomonas bernginesa PA01, an opportunistic pathon A; Reference number: A82956; Mujb; 2043737; PMTD: 10944013
A; Reference number: A82956; Mujb; 2043737; PMTD: 10944013
A; Status: prelumnary
A; Molecule Lype: DMA
A; Residues: 1-397 < SIO;
A; Cross-references: GH: ABC00695; GH: ABC04091; NID: 9994R736; PIDM: AAG 1: GSPUH: GNCC;
C; Genetics: A; Gene: FA2662
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                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.6%; Pred. No. 1.36+62;
Matches 5; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jength 397:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Shmilarity 55.6%: Fred. No. 1.56+02;
Matches 5; Conservative 3; Mishatches 1; Indels
A)Gene: GDB:FLEX; p47
A;Cross-references: GDB:9836816; GMIM:173570
A;Map position: 2pter-2qter
C;Superfamily: pleckstrin; pleckstrin; repeat homology
C;Keywords: phosphoprotein; signal lransdiction
F;3-99/Domain: pleckstrin repeat homology <PLK1>
F;243-345/Domain: pleckstrin repeat homology <PLK2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: September 29, 2003, 19:06:56
Job Lime : 22 secs
                                                                                                                                                                                                                                                                                                                                                                                                       292 LRGCVVTSV 300
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QC
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 29, 2003, 18:58:47; Search time 10 Seconds Run on:

(without alignments) 42.324 Million cell updates/sec

US-09-965-594-1\_COPY\_14\_22 Title: Perfect :

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 LIGGIIISI 9 score: Scoring table: Sequence:

127863 segs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 99% Listing first 45 summaries

SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		œ			SUMMARIES		
Result No.	Score	Query	Len	ia ia		ription	
	43	6		` !	POLG_ROV.T	0.00269 h qenome po	
2	7.0	6.05				h denome	
٣	(C)	87.8			T2R9_MOUSE	mas mason	
77	3.5	79.5	653		EGUN_PIG	237176 sus serofa	
S	34	77.3			YBI6_YEAST	Sacc	
9	33	75.0			T2R7_HUMAN	۳.	
7	33	75.0			PLEK_HUMAN	P08567 homo sapien	
œ	ε Ε	75.0			PLEK_MCUSE	BULS. E	
Q	33	75.0			ARGD_PSEPK	psen	
10	33	75.0			FLHF_PSEFU		
11	33	75.0			YBBE_BACSU		
12	33	75.0			SYFB_SHEON		
13	33	75.0		_	PGDS_HUMAN	P16234 homo sapien	
14	33	75.0			DICE_MOUSE		
15	33	75.0			DICE_HUMAN		
16	32	72.7			PSD9_RAT	ratto	
17	32	72.7			REIS_TODPA	todarodes	
18	3.5	72.7			KDGT_BACSU		
79	32	72.7			YJGN_ECOLI	escherich	
<b>5</b> 0	32	72.7			RAPS_CHICK	O42393 gallus gall	
21	32	72.7			AGAL_MOUSE		
22	32	72.7			GHT2_SCHPO		
23	32	72.7			TGM2_CAVCU		
24	32	72.7			YDG1_SCHPO		
52	32	72.7			SM5A_HUMAN	Q13591 homo sapien	
56	32	72.7			SMSA_MOUSE	O62217 mus musculu	
27	31	70.5			SSRP_NEIMA		
88	31	70.5			IL15_BOVIN	scq	
58	31	70.5			SP22_MOUSE	som som d	
30	31	70.5			LAPT_PASHA	bas≎	
31	31	76.5			MCA1_HUMAN		
32	31	70.5		_	T2R6_MOUSE	P59530 mus muscula	
	31	70.5		_	YMI7_YEAST	٥	

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EMBL; D11168; BAA01943.1; -.

InterPro; IPR301410; DEAD.

PDB; 1A10; 25-MAR-98, PDB; 1JXP; 14-JAN-98, MEROPS; S29.001; MEROPS; U39.001; PIR: A45573; A45573

3.5	7.07		-	avasa ason	
			4	1006_robot.	CATE DESCRIPTIONS
35 31	70.5		-	YJGN_ECO57	P58219 escherichia
36 31	70.5		• •	RAPS_HUMAN	013702 homo sapien
37 31	70.5	411	٦	RAPS_MOUSE	
38 31			٦	RAPS_TORCA	P09108 torpedo cal
			r 4	PCL_RHOCA	C69140 rhodobacter
			rH	ETIR_PIG	Q29010 sus scrofa
41 31			٦	Y326_METJA	Q57772 methanococc
42 31			-	IOLF_BACSU	P42417 bacilius su
43 31			~	POLG_DEN23	P14339 denque viru
44 31			٦	PT1_STRCO	Q9kzpl streptomyce
45 31			7	THI3_YEAST	007471 saccharomyc
				ALIGNMENTS	
RESULT 1 POLG_HCVUT					
		CO COLO		2000	

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POLG_BCVJT STANDARD; PRT; 301C AA.
0,00263.
0.1APP-1993 (Rel. 25, Created)
0.1APK-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updato)
05-One polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein El (GP3) (GP3); Ervelope glycoprotein El (GP6) (GP6) (GP70) (NS1); Protein P7; Norstructural protein NS2 (P21)
(EC 3.4.22-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21-9); Nonstructural protein NS4A (P4); Nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infected individuals...;
Virus Res. 23.39'55(1992).
Virus Res. 23.39'55(1992).

**PUNCTION: TIE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE NEWHRANE-RELATED FUNCTION.

**NS AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

**NS AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

**IT CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral procursor polyprotesin, commonly with Asp or Giu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.

**POSITION.**CYS OF THE IN P1 and Ser or Ala in P1'.

**IT CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + ONTALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + ONTALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + ONTALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + ONTALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + ONTALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + ONTALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + ONTALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + ONTALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + ONTALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + ONTALYTIC ACTIVITY: N nucleoside triphosphate + ONTALYTIC ACTIVITY: N nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-92295714: PubMed-1318627;
Tanaka I., Kato N., Nakagawa M., Ootsuyama Y., Cho M.J.,
Tanaka I., Kato N., Ishimara Y., Shimotomo K.;
"Molecular Cloning of hepatitis C virus genome from a single Japanese carrier: sequence variation within the same individual and among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCULT: THE VIRTON OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M. AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C. AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                NS4B (P27): Nonstructural protein NS5A (P56): Nonstructural protein NS5B (P66) (P70) (RNA-directed RNA polymerasc) (EC 2.7.7.48)]. Hepatitis C virus (isolate HC-JT) (HCV). Viruses: SSRNA positive-strand viruses, no DNA stage: Flaviviridae; Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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1039 LLGCIVISL 1047
                                    RESULT
                                                                                                                                                                                                                                                                   CAPSID PROTEIN C (POTENIAL).
MATRAY PROTEIN (POTENI'AL).
MAJOR ENVELOPE PROTEIN E (SOTENIAL).
NONSTRUCTURAL PROTEIN NS1/E2 (POTENIAL).
NON STRUCTURAL PROTEIN NS2 (POTENIAL).
PROTEASE/HELICASE NS3 (POTENIAL).
NONSTRUCTURAL PROTEIN NS4A (POTENIAL).
NONSTRUCTURAL PROTEIN NS4B (POTENIAL).
POTENIAL).
POTENIAL.
                                                                                                                                                                                                                  Polyprotoin: Glycoprotein: Transferase, RNA-directed RNA polymoruse;
Core protein: Coat protein: Envelope protein; Helicase: ATF-binding;
Transmembrane: Nonstructural protein; Hydrolase: Serine protease:
                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                    REMOVED FROM CAPSID PROTEIN C BY THE CELEULAR AMINOPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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Pred. No. 5.9;
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DECH BCX.
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                                                                                   IPR007095; RNA_pol_US_PS.
IPR007094; RNA_pol_PSvir.
543; HCV_capsid; 1.
542; HCV_core; 1.
                                                                    HCV_NS5a.
HCV_RdRP.
                                          HCV_NS3.
HCV_NS4a.
                                                            HCV_NS4b.
                                                                                                                                                      Pfam, PF01006, HCV_NS4a: 1.
Pfam, PF01001; HCV_NS4a: 1.
Pfam; PF01506: HCV_NS5a: 1.
Pfam; PF01506: HCV_NS5a: 1.
Pfam: PF01506: HCV_NS5a: 1.
Pfam: PF019098: Viral_RFP: 1.
Probom: PD186562; HCV_NS1; 1.
SMART: SMG487; DEXDC: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326573
                                                                                                                      HCV_env; 1.
HCV_NS1; 1.
HCV_NS2; 1.
HCV_NS3; 1.
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1006
1615
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2013
3010
369
1083
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                                          IPR002531;
IPR002518;
                                                                             IPR002166:
                                                                    IPR002869;
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                                                                                                                                                                                                                                                                                                                                                                                PF01560;
PF01538;
                                                                                                      Pfam; PF01543;
Pfam; PF01542;
                                                                                                                       PF01539;
                                                                                                                                               PF02907;
                                                                                                                                                                                                                                            3D-structure.
INIT_MET
                                           InterPro;
InterPro;
                                                            fiterPro;
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                          InterPro;
                                    interPro;
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                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
01-APR-1993 (Rel. 42, Last amondation update)
Gence polyprotein: Contains anotation update)
Gence polyprotein: Contains (GPS3) (GPS3); Envelope glycoprotein E2
(GPS8) (GPP0) (NS1); Protein P7: Nonstructural protein NS2 (GPS3) (GPS3); Envelope glycoprotein E2
(GPS3) (GPP0) (NS1); Protein Protein NS4 (P4); Nonstructural protein NS54 (P7); Nonstructural protein NS54 (P5); Nonstructural protein NS54 (P5); Nonstructural protein NS54 (P6) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48);
Hepatitis C virus (isolate Taiwan) (HCV).
                                                                                                                                                                                                                                                                                   ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29
               3010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001410; DEAD.
Interpro; IPR00252; HCV_capsid.
Interpro; IPR00252; HCV_capsid.
Interpro; IPR002519; HCV_env.
Interpro; IPR002519; HCV_env.
Interpro; IPR002519; HCV_env.
Interpro; IPR002519; HCV_NS2.
Interpro; IPR001409; HCV_NS3.
Interpro; IPR001409; HCV_NS4.
Interpro; IPR001045; HCV_RGMP.
Interpro; IPR001049; RNA_pol_DS_PS.
Interpro; IPR007095; RNA_pol_DS_PS.
Interpro; IPR007094; RNA_pol_DS_PS.
Interpro; IPR007094; RNA_pol_PSvir.
Pfam; PP01543; HCV_Core, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: M84754; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1N64; 25-FEB-03.
PDB; 1N53; 08-APR-98;
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                                                                                                                                                                                                                                          Hepacivirus.
NCBI_TaxID=31645;
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MEROPS; U39.001;
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POLG_HCVTW
ID POLG_HCVTW
AC P29846;
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0

Gaps

.. 0

Indels

Mismatches

Conservative

.. 89

Matches

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musculus (Mouse).
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                                                                                                              CELLULAR AMINOPEPTIDASE.

CORE PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS1/92 (POTENTIAL).

PROTEINS (POTENTIAL).

PROTEINS (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                 RNA-DIRECTED RNA POLYMERASE (POTENTIAL)
POTENTIAL:
                                                                           Polyprotein, Glycoprotein, Transferasc, RNA-directed RNA polymerasc, Core protein, Coat protein, Envelope protein, Helicasc, ATP-binding; Transmembrane, Nonstructural protein, Hydrolasc, Serine protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Taste receptor type 2 member 9 (T2R9) (Taste receptor type 2 member
1AS2R5).
                                                                                                         REMOVED FROM CAPSID PROTEIN C BY THE
                                                                                                                                                                                                CHARGE RELAY EYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                            Sength 3010;
                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                   N-11NKED GLCNAC.
                                                                                                                                                                                                                                                                                             N-LINKED (SIGNAC)
                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
21;
                                                                                                                                                                                                                                                                                                     (SLCNAC.
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-LINKED (GLCNAC.
-LINKED (GLCNAC.
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DECH BOX.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
PF01560; HCV_NS1; 1.
PF01538: HCV_NS2; 1.
PF02057; HCV_NS3; 1.
PF01006; HCV_NS43; 1.
PF01001; HCV_NS43; 1.
PF01506; HCV_NS53; 1.
PF00271; helicase_C: 1.
PF00998; Viral_RGRP; 1.
                                                                                                                                                                                                                                                        90.98;
                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFGCIITSL 1047
                                                                     SMART; SM00487; DEXDC;
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LLGCIITSL 9
                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
                      Pfam; PF01006; H
Pfam; PF01001; H
Pfam; PF01506; H
Pfam; PF00271; h
Pfam; PF00998; V
                 PF02967;
         PF01538;
                                                                                                 3D-structure.
INIT_MET
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Q9JKT4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1039
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ACT_SITE
ACT_SITE
NP_BIND
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                 Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discriminate among bitter stimuli.
-!- SIMILARITY: Belongs to family T2R of G-prolein coupled receptors.
-!- COUTION: This protein was previously referred to T2RS, but due to its high similarity towards both the human and rat T2R9 sequences it is considered to be T2R9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells of the tonque and palate epithelium and exclusively in quistducinpositive cells. Expressed in quastric and duodenal tissues.

MISCELLANEOUS: Mast easte cells may be activated by a limited number of bitter compounds; individual taste cells can
                                                                                                                                                                                                                                                                                                                                                                                                                                       Adler E., Feng L., Guo W.,
Eukaryota: Metaria; Chordata: Craniata; Vertebrata: Euteleostomi:
Mammalia: Eutheria; Rodentia: Sciurognathi: Muridae; Murinac; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                             Ryba N.J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Margolskee R.F.; "Molecular mechanisms of bitter and sweet taste transduction."; J. Biol. Chem. 277:1-4(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                           MEDLINE-20222571; PubMed-10761934;
Adler E., Hoon M.A., Mueller K.L., Chandrashekar J.,
Zuker C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor: G-protein coupled receptor; Transmembrane
                                                                                                                                                                                                                                                                                     "A novel family of mammalian taste receptors.";
Cell 100:693-762(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zuker C.S., Ryba N.J.,
"T2Rs function as bitter taste receptors.";
Cell :00:703-711(2000).
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-20222572; Pubmed-10761935;
Chandrashekar J., Muclier K.L., Hoon M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monthwayeur J.-P., Matsunami B.;
"Receptors for bitter and sweet taste.";
Curr. Opin. Neurobiol. 12:366-371(2062).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-22135574; PubMed-12139982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEDLINE-21634924; PubMed-11696554;
                                                                                                                                         SEQUENCE FROM N.A., AND TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF227147; AAF43920.1; -. Pfam: PF05296; TAS2R: 1.
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43
64
87
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YBT6_YEAST
P38250;
                                                                                CARBOHYD
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                                                               CARBOHYD
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SITE
      DOMAIN
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T2R7_HUMAN
                                                                                                                                                                                                                                                                                                                                              YBT6_YEAST
                                                                                                                                                                                                                                                                                                                             RESULT
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      SO FEET SO
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                                                                                                                                                                                                                                                                                                     ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       functions afforming growth factor-beta.";
J. Biol. Chem. 269:1995-2001(1994).

-!- FUNCTION: MAJOR GLYCOPROTED.
-!- FUNCTION: MAJOR GLYCOPROTED. OF ENDOTHELIUM. MAY FLAY A CRITICAL ROLE: IN THE BINJING OF ENDOTHELIAL CELLS TO INTEGRINS AND/OR OTHER RGD RECEPTORS.
-!- SUBUNII: HOMODIMER THAT FORMS AN HETEROMERIC COMPLEX WITH THE SIGNALING RECEPTORS FOR TRANSFORMING GROWTH FACTOR-BETA: TGF-BETA RECEPTORS I AND/OR II. IT IS ABLE TO BIND TGF-HETA 1, AND 3 EFFICIENTLY AND TGF-BETA 2 LESS EFFICIENTLY.
-!- SUBCELLULAR MOORTION: Type I membrane Protein.
-!- SUBCELLULAR MOORTION: Type I membrane Protein.
-!- SIMILARITY: SOME REGIONS OF SIMILARITY TO TGF-BETA RECEPTOR TYPE III (BETAGLYCAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endoglin forms a heteromeric complex with the signaling receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostumi;
Mammalia; Eutheria; Cetarticdactyla; Suina; Suidae; Sus.
                                                                                                                                                                                          92AD449C68Fb85FB CRC64;
                                                                                                                                                                                                                                                                                                     ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamashita H., Ichijo H., Grimsby S., Moren A., ten Dijke P.,
Miyazono K.;
                                                                                                                                                                                                                                                           Score 36; 38 1; Length 360;
Pred. No. 16;
2; Mismatches 0; Indels
                CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
5 XTARCELLUIAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
6 (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELIBLAR (POTENTIAL) POTENTIAL.
                                                                                                                                                              7 (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane, Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-001-1994 (Rel. 30, Created)
01-00T-1994 (Rel. 36, Last sequence update)
28-FEB-2063 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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Pfam: PF00100; zona_pellucida; 1.
SMART: SM00241; 2P: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94124550; PubMed-8294451;
                                                                                                                                                                                                                         34416 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell adhesion; Glycoprotein:
                                                                                                                                                                                                                                                             81.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: 223142; CAA80673.1; -.
PIR; A49722; A49722.
                                                                                                                                                                                                                                                               81.8
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    133 LLGCLLTS 140
                                                                                                                                                                                                                                                                                                                                              1 LLGCIIIS 8
Endoglin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                           DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                       DOMAIN
TRANSMEM
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  TRANSMEM
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EGLN_PIG
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Mannhaupt G., Stucka R., Ehnle S., Vetter I., Feldmann H.;
"Analysis of a 70 kb region on the right arm of yeast chromosome II.";
Yeast 10:1363-1381(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                       Gaps
                         SER/THR-RICH.
CELL, ATTACHMENT SITE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                               N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1994 (Rel., 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 105.9 kDa protein in AAC3-RFC5 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB i; Length 946;
Pred. No. 96;
                                                                                                                                             DB 1; Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105903 NW; F51A43A5D378B7BC CRC64:
                                                                                  N-LINKED (GLCNAC. . .) (PO
788784A61DFE3E5A CRC64;
      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                     946 AA
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                             Score 35;
Pred. No. 4
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TRANSMEM 122 142
                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                             79.5%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.3%;
653
574
400
57
306
70279 %
                                                                                                                            Query Match
Best Local Similarity 87.5.
the 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 52.5
Matches 5; Conservative
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| 520 ILGCVITA 527
                                                                                                                                                                                                                                                   111 ||||
379 LGCTIISL 386
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      607
335
396
57
306
653 AA;
                                                                                                                                                                                                                           2 LGCIITSL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YBROBEC OR YBR0809.
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STRAIN-S288C;
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2218
2254
303
4448
564
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PS50262;
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                   Receptor;
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TRANSMEM
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TRANSMEM
                                            IRANSMEM
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   PROSITE;
                                                                                                          PRANSMEM
                                                                                                                                         TRANSMEM
                                                                                                                                                                       TRANSMEM
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                                 DOMAIN
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PLEK_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bitterness and is gustducin-linked. May play a role in sensing the chemical composition of the gastroincestinal contest. The activity of this receptor may stimulate alpha gustducin, mediate PLC-beta-2 activation and lead to the gating of TRPMS.
SUBCEMBLUAR LOCATION: Integral membrane protein.
TISSUS SPECIFICATION: Integral membrane protein.
of the tongue and palate epitholium and exclusively in gustducin.
                           15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
13-Set roceptor type 2 member 7 (12R7) (Taste receptor family H member
4) (TRB4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to family T2R of G.protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang Y., Hoon M.A., Chandrashekar J., Mueller K.L., Gook B., Wu D., Zuker C.S., Ryba N.J.;
Zuker C.S., Ryba N.J.;
"Coding of sweet, bitter, and umami tastes: different receptor cells sharing similar signaling pathways.";
Cell 112:293-301(2003).
                                                                                                                                                                                                                                                                                                                       MEDLINE-2022552; PubMed-10761935;
Chandrabekar G., Mueller K.L., Hoon M.A., Adler E., Feng L., Guo
Zuker C.S., Ryba M.J.;
"T2Rs function as pitter taste receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANDOUS: Most taste cells may be activated by a limited number of bitter compounds; individual taste cells can discriminate among bitter stimuli.
                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Entelcostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                  J., Ryba N.J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Margolskee R.F., Molecular mechanisms of bitter and sweet taste transduction.", J. Biol. Chem. 277:1-4(2002).
                                                                                                                                                                                                                               Adler E., Hoon M.A., Mueller K.L., Chandrashekar
Zuker C.S.;
                                                                                                                                                                                                                                                             "A novel family of mammalian taste receptors."; Cell 100:653-702(2000).
318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Montmayeur J.-P., Matsusami H.;
"Receptors for bitter and sweet taste.";
Curr. Opin, Neurobiol, 12:366-371(2002).
                                                                                                                                                                                                 SEQUENCE FROM N.A., AND TCPCLOGY.
MEDLINE=20222571; Pubmed-10761934;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22135574: PubMed-12139982;
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Pfam; PF05296; TAS2R; 1.
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               positive cells.
MISCELLANEOUS: N
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F2R7_HUMAN
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                                                                                                          TAS2R7
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Attausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Haha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata: Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-882329;0; PubMed-2897530;
Tyers M., Rachubinski R.A., McCaw M.L., Varrichio A.M.,
Shorr RG.L., Haslam R.J., Harley C.B.;
"Molecular cloning and expression of the major protein kinase C
substrate of platelets.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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*Molecular analysis of picckstrin: the major protein kinase C
**notrarts of natabate "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 1; Length 318,
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2 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                               4 (POTENTIAL).
EXTRACELLULAR (POIENTIAL)
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                       3 (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
                                                                                                                CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 59;
3; Mismatches
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J. Cell. Biochem. 40:133-145(1989)
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Best Local Similarity 55...
5: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substrate of platelets.";
Nature 333:470-473(1988).
                                                                 134 LLGCVVLSV 142
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                                      G-protein
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167
175
318 AA;
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DOMAIN
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       Sanchez A.,
                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 1-105.

WINDLINE-9426857; Pubmed-8208296;
YOON H.S., Hajduk P.J., Petros A.M., Olejniczak E.I., Meadcws R.P., Fesik B.W.;
Fesik S.W.:
Fesik S.W.:
Fesik B.W.:
Fesik B.
Fahey J., Helton E., Kotteman M., Madan A., Rodrigues S., Sanchoz Whiting M., Madan A., Young A.C., Shevchenko T., Bouffard G.G., Blakesley R.W., Cuchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimmood J., Schmutz J., Myers R.R., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schneroft A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and intial analysis of more changed full length human and mouse cDNA sequences.
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63:
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40082 MW; ZEZA128C8B526361 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60) GO:0005509; F:calcium ion binding activity: TAS.
InterPro: IPR000591; DEP.
InterPro: IPR001849; PH.
                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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PH 2.
W -> R.
/FTId-VAR_005524.
N -> K (1N REF. 3)
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Pred. No. 6
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Pfam; PF00169; PH: 2.
SMART; SM00049; DEP: 1.
SMART; SM00033; PH: 2.
PROSITE: PS50186; DEP: 1.
PROSITE; PS50003; PH_DOMAIN: 2.
Phosphorylation; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X07743; CAA30564.1; -. EMBL; BC018549; AAH18549.1; -. PIR; S00755; S00755.
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Best Local Similarity 55.
5; Conservative
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MIM; 173570; -.
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350 AA;
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VARIANT
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                                                                                                       Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Euthazoa: Chordatia; Sciuroquathi; Maridae: Murinae; Mus-
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAJOR PROFEIN KINASE C SUBSTRATE OF PLATELETS, IIS
EXACT FUNCTION IS NOT KNOWN.
-!- SIMILARITY: Contains 1 DEP domain.
-!- SIMILARITY: Contains 2 PH domains.
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                                                                                                                                                                                                                                                                                                                                                                                                    Abn H.-J., Cho J.-J.;
"Mouse pleckstrin 1 is induced in mast cells after 19E cross-
                                                                                                                                                                                         STRAIN-BALB/C;
MEDLINE-20318622; PubWcd-10860665;
Cmark J.L., Hegamyer G., Gerrard B., Dean M., Colburn N.H.;
"cDNs cloning and mapping of mouse pleckstrin (Plek), a gene uprequiated in transformation-resistant cells.";
Genomics 66:204-212(2000).
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PH 2.
LH 2.
L - 2 (IN REF. 3).
F -> L (IN REF. 3).
W; 348F3CB469B7CC53 CRC64;
                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
PI.EK_MOUSE STANDARD; PRI; 350 AA. 09JHK5; 09FR19; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 33; DB 55.6%; Pred. No. 63; tive 3; Mismatches
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PROSITE; PS50003; PH_DOMAIN;
Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1860485; Plek,
InterPro; IPR060591; DEP.
InterPro; IPR001849; PH.
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Pfam; PF00169; PH; 2.
SMART; SM00049; DEP; 1.
SMART; SM00233; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 3
120 1
225 2
350 AA;
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
                                                                                                                                                                             SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=10090;
                                                                          Pleckstr;n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  linking.
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DOMAIN
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1 LLGCIITSI 9

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Caps

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Tacels

Mismatches

1 1.::11: 292 LRGCVVTSV 300 1 LLGC: 1TSL 9

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NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                      STRAIN-PRS2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YBBE_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
NP_BIND
SEQUENCE
                                                                                                                              protein).
                                                                                                                                                                                                                                                                                                           SECTENCE
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YBBE_BACSU
SETERES NO CONTRACTOR OCCOUNTS NO CONTRACTOR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and tor commercial entities requires a license agreement (See http://www.tsb-sib.ch/announce/or send an email to licensedisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabolically versatile Pseudomonas pulida KT2461.)

Environ, Microbiol, 4:799-808(2022)

-!- CATALYTIC ACITVITY: N(2)-8emialdoxyde + 2-qlutarate - N-acetyl-L-glutamate S-semialdoxyde + 2-qlutarate.

-!- COFACTOR: Pyridoxal phosphate (Hy similarity).

-!- PATHWAY Actinine blosynthesis: lourth step.

-!- MISCRILANEOUS: May also have succiny diaminopimelate aminotransferuse activity, thus carrying out the fourth step in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to class-III of pyridoxal phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDINE=242366; PubMed=12534463;
Nelson K.E., Weincl C., Paulson T.T., Dodson R.J., Hilbert H.,
Nelson K.E., Weincl C., Paulson T.T., Dodson R.J., Hilbert H.,
Martins dos Sancos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac C., Beenan M., White O., Peterson J., Khouri H., Hanco I.,
Madupu R., Nelson W., White D., Foutson D., Tran K., Moazzez A.,
Otterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tucmmler E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyridoxal phosphate; Complete proteome.
BINDING 255 255 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                        Pseudomonas putida (strain KT2443).
Bacteria: Proteobactoria: Garmaproteobacteria; Pseudomonadales;
Pseudomonadaceae: Pseudomonas.
NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence and comparative analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5597D2F10C3E221E CRC64;
                                                                                                                                                                                                  28-FEB-2003 (Re). 41, Created)
28-FEB-2003 (Rec). 41, fast sequence update)
15-SEP-2003 (Rel, 42, Last annotation update)
Acetyioznithine aminotransferase (EC 2.5.1.11) (ACOAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAKAP: MF_C1107; -: 1.
Priam: PF02202; am:notran_3; 1.
TIGRFAMS: TIGRO70707; argp; 1.
PROSTITE; PS00606; AA_TRANSFR_CLASS_3: 1.
Arginine biosynthesis; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 M.
                                                                                                                                                      405 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMB1: AEC16790; AAN70056.1: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 AA; 43490 MW;
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Best Local Similarity 71.4 Matches 5; Conservative
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                        292 LRGCVVISV 300
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ARGD OR PP4481.
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P59319:
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                                                                                                                              ARGC_PSEPK
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                                                                                                      RESULT 9
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                                                                                                                                                                                                                                                                                                                                                  Ditty J.L., Grimm A.C., Harwood C.S.;
Fidentification of a chemotaxis gene region from Pseudomonas putida.";
FEMS Microbiol. Lett. 159:267-273(1998).
-: FUNCTION: NECESSARY FOR FLAGELLAR BLOSYNTHESIS. MAY BE INVOLVED
IN TRANSLOCATION OF THE FLAGELLUM (BY SIMILARITY).
-: SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROIEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97419514; PubMed-9274029;
Liu H., Haga K., Yasumoto K., Ohashi Y., Yoshikawa H., Takahashi H.;
"Sequence and analysis of a 31 kb segment of the Bacillus subtilis
chromosome in the area of the rrnH and rrnG operons.";
Microbiology 143:2763-2767(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saps
is-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last anotation update)
Flagellar biosynthesis protein flik (Flagella associated GTP-binding
                                                                                                                                                                      bacteria: Profeobactoria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBL_IaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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66.7%; Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (RY SIMILARITY).
EBF1A6A650B9B27A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                005213; 008069; Q45578; 28-FEB-2003 (Rei. 41, Created) 28-FEB-2003 (Rei. 41, Last sequence update) 48-FEB-2003 (Rel. 41, Last annotation update) Hypothetical protein ybbE precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRP54; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro: IPR003593; AAA_Arpase.
Interpro: IPR0008597; SRP54,
Pram: PF00448; SRP54, 1.
Profom: PF02881; SRP54, 1.
Profom: P7000819; SRP54, 1.
PROFITE; P800082; AAA, PRE_NEC_NEC
                                                                                                                                                                                                                                                                                                                                  MEDLINE-98164359; PubMed-9503621;
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437 AA; 47512 MW;
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Best Local Similarity 66.7
Matches 6, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flagella, GTP-binding
NP_BIND 225 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LIGCIITSL 9
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                                                                                                                                                         Pseudomonas putida
                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis
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15.SEP-2003 (Rel. 42, Created)
15.SEP-2003 (Rel. 42, Last sequence update)
15.SEP-2003 (Rel. 42, Last amortation update)
15.Pepylalapyl-TRNA syntherase beta chain (EC 6.11.20)
(Phenylalanine--tRNA ligase beta chain) (PheRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
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                                                        A Kunst F., Ogasawara N., Mosker I., Albertini A.M., Alloni B.,

A Accede V., Hertero M.S., Bessieres P., Felotin A., Borchert S.,

A Accede V., Hertero M.S., Bessieres P., Felotin A., Borchert S.,

A Brouillet S., Bruschi C.V., Caldeell B., Capudno V., Carter N.M.,

A Brouillet S., Brington J.J., Concerton I.F., Cummings N.S., Daniell R.A.,

Choi S.K., Codani J.J., Concerton I.F., Cummings N.S., Daniell R.A.,

Brian K.D., Errington J., Ferna S., Galtzin B.D., Calleron N.,

A Drian K.D., Errington J., Ferna S., Galtzin B.D., Calleron N.,

R. Hibert H., Gasappel S., Hoseno S., Hulle M.F., Leanerson P.I.,

A Joris B., Karamata D., Kasahara Y., Raerr Blanchard M., Klein G.,

A Joris B., Karamata D., Kasahara Y., Klearr Blanchard M., Klein G.,

A Joris B., Karamata D., Kasahara Y., Raerr Blanchard M., Klein G.,

A Joris B., Karamata D., Rasahara Y., Roetter P., Koningstein G., Krogfs S., Kundro M.,

A Lee S.M., Levine A., Liu E., Masuda S., Wangel C., Redigne C.,

Redina N., Mcledo R.P., Mizuno M., Mossil D., Nakai S., Nchack M.,

Reger M., Rivolta C., Roche B., Roche B., Rose M., Sadaie Y.,

Rateconi M., Rivolta C., Roche B., Roche B., Rose M., Sadaie Y.,

Sarloun D., O'Reilly M., Ogawa K., Ogiwara A., Cidoga B., Park S.H.,

Rateconi E., Pujic P., Purnolle B., Roche B., Rose M., Sadaie Y.,

Sarloun M., Tamakoshi A., Tanaka I., Takahashi E., Takemaru K.,

Takeuchi M., Tamakoshi A., Tanaka I., Takahashi E., Yasamoto R., Vasamoto R., Varien P., Haller B., The Complete genome sequence of the Gran-positive bacterium Bacillus The Daniella R., The Complete Genome sequence of the Gran-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE UPF0214 FAMILY. CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 33; DB 1; Length 441; 66.7%; Pred, No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL PROTEIN YBBE. A90FD2APC9015517 CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: AB302150: BAA19500.1: ALT_FRAME.
EMBL: AB302150: BAA19501.1: ALT_FRAME.
EMBL: 299104: CAB31943.1: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                     STRAIN-168;
MEDLINE-98044033; PhbMed-9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 AA; 49304 MW:
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nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390:249-256(1997)
   (2)
SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLUIÂR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the phenylalanyi-tRNA synthetasc beta chain
                                                                                                                                                                                                                 Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Isapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Wadupu R., Peterson J.D. Cmayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Tmpraim M., Loc K., Berry K., Lee C., Mieler T.V., Smith H.C., Venter J.C., Nealson K.H., Fraser C.M., Schome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
Metal-binding; Magnesium; RNA-binding; tRNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MAGNESIUM (VIA CARBONYL CXYGEN) (BY
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0
                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Alteromomadales;
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Pred. No. 1.3e-02;
---hes 0; Indels
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MAGNESIUM (BY SIMILARITY).
D73CD96D4CAE1296 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family. Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRNA-BINDING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03147; FDX-ACB; 1.
Pfam; PF01588; tRNA_bind; 1.
TiGRFAMs; TiGR00472; phcT_bact; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; SO2086; -. HAMAP; MC_00283; -; 1. InterPro; IPR005146; B3_4. InterPro; IPR005147; B5. InterPro; IPR005121; Fdx-AntiCB. InterPro; IPR005121; Fdx-AntiCB. InterPro; IPR005123; Phor_bact. InterPro; IPR005547; tRNA_bind. Pfam; PP03483; B3_4; I. Pfam; PP03484; B5; I.
                                                                                                                                                                                                    MEDIJNE-22297685; PubMed-12358813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE015650; AAN55133.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 M. M. 86574 MW;
                                                           Alteromonadaceae; Shewanella.
NCBl_TaxID=70863;
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                        Shewanella oneidensis.
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Best Local Similarity
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795 AA;
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PHET OR SOZ085
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RESULT 12

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CARBOHYD
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EMB1;
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EMBL;
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      KARARANANAN BERMANAN BERMAN BERMAN BERMANAN BERMANAN BERMANAN BERMANAN BERMANAN BERM
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                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annoration update)
Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112)
(PDGF-R-alpha) (CD140a antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDINE-89130149; Pubmed-2536956;
Matsui T., Heidaran M., Mixi T., Popescu N., is Rochelle W.,
Kraus M., Pierce J., Aaronson S.,
*Isolation of a novel receptor cDNA establishes the existence of two
PDGF receptor genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure, organization, and transcription units of the human alpha-platelet-derived growth factor receptor were, PDGFRA."; Genomics 30:24-232(1995).
-!- FUNCTION: THIS PROCEPTOR BINDS PLATELET-DERIVED GROWTH FACTOR AND HAS A TYROSINE-PROTEIN KINASE ACTIVITY. THIS RECEPTOR CAN BIND BITHER PDGF-A OR PDGF-B.
-!- CATALYTIC ACTIVITY: AIP - a protein tyrosine - ADF + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claesson-Weish L., Eriksson A., Westermark B., Holdin C.H.:
"DNA cioning and expression of the humar A-type platelet-derived
growth factor (PDGF) receptor establishes structural similarity to
the B-type PDGF receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
SUBUNIT: DIMER OF EITHER ALPHA-ALPHA, BRIA-HETA OR ALPHA-BEIA
                                                                                                                                                                                                                                                                                            Eukaryola; Melazoa; Chordata; Cranhata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
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                                                                                                                      1089 AA
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MEDLINE-96163874; PubMed-8586421;
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BAA08742.1; -.
BAA08742.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 243:800-804(1989).
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                                                                                                                      STANDARD;
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591 MEGCVIT 597
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P16234;
                                                                                                                                                                                                                                                           PDGFRA
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                                                                              RESULT 13
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N-LINKED (GLCNAC. ) (POTENITAL).

N-LINKED (GLCNAC. ) (POTENITAL).
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R INTERPORT I PRO00306: 19_MHC.

R PRO00306: 19_MHC.

R PRO00317 19_MHC.

R PROSTIE; PSO00401: 19_MHC.

R PROSTIE; PSO00101: PROTEIN_KINASE_DOM; 1.

R PROSTIE; PSO00101: PROTEIN_KINASE_DOM; 1.

R PROSTIE: PSO00102: PROTEIN_KINASE_DOM; 1.

R PROSTIE: PSO00401: RECEPPIOR_TYRK.III: 11.

R PROSTIE: PSO00401: RECEPPIOR_TYRK.IIII: 11.

R PROSTIE: PSO00401: RECEPPIOR_TYRK.IIII: 11.

R PROSTIE: PSO0
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ATP (BY SIMILARITY).
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IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
FROIEIN KINASE.
SER-RICH.
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Pred. No. 1.6e+02
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ID DICE_MOUSE STANDARD: F
AC 08R418:
DT 28-FEB-2003-(Rel. 41, Created)
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| D50010; BAA08742.1; J
| D50011; BAA08742.1; J
| D50012; BAA08742.1; J
| D50013; BAA08742.1; J
| D50014; BAA08742.1; J
| D50016; BAA08742.1; J
                                                                                                                                    EMBL: D50015; BAA08742.1; J
EMBL: D50016; BAA08742.1; J
PIR: A40162; PFHUGA.
FSSP: P11362; IFGK.
Genew; HGNC:8803; PDGFRA.
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Best Local Similarity 55.0.
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SMART; SM00535: RIBOC; 2.
PROSITE; PSS0137: DAZ: 1.
PROSITE; PSS0121: PAZ: 1.
PROSITE; PSS0142; RNASE 3.
PROSITE; PSS0142; RNASE 3.
PROSITE; PSS0142; RNASE 3.2; 2.
Helicase; ATP-binding; RNA-binding; Hydrolase; Endonuclease;
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SIMILARITY: BELONGS TO THE HELICASE FAMILY.
SIMILARITY: Contains 2 Ruses III domains.
SIMILARITY: Contains 1 PAZ domain.
SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
                                                           ribonuclease fDCR-1).
DICBRI OR DICEK OR MBCR.
Bukar musculus (Mouse).
Eukaryota: Metazoa: Chordata: Craniata: Vortebrata: Eutoleosiomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Mus.
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Saigo K.;
Eff2C family protains and Dicer homologs are required for siRNA mediated RNAi in mammalian cells."
Submitted (MAR-2002) to the EMBL/GenBank/DBUJ databases.
-!- FUNCTION: Involved in Cleaving double-stranded RNA in the RNA interference (RNA) patiway. It produces 21 to 23 bp dsRNAs (siRNAs) which target the selective destruction of homologous
                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Czech II;
Svoboda P., Anger M., Stein P., Schultz R.M.;
"Mouse dicer bomolog in cocyte and preinglantation umbryos.";
Submitted (OCT-2001) to the EMBL/GenBank/DDRJ databases.
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endoribonuclease Dicer (BC 3.1.26.-) (Bouble-strand-specific
                                                                                                                                                                                                                           MEDLINE-21886641; Pubmed-11889553;
Nicholson R.H., Nicholson A.K.;
Molecular characterization of a mouse cDNA encyding Dicer,
ribonuclease III ortholog involved in HNA interference.";
Mamm. Genome 13:67-73(2002).
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EMBL, AF430845; AAR21495.1; ALT_INIT.
EMBL, AB061470; BAC1575.1; -
MGD, MGT:2177.78; Dicerl.
InterPro: IPR001410; DSAD.
InterPro: IPR001410; DSAD.
InterPro: IPR00159; OS_ERB.
InterPro: IPR001656.3; DELGase_C.
InterPro: IPR00100; PAZ.
InterPro: IPR0010099; RN4Se_3.
PEam: PF00170; DEAD.
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SMART; SM00487; DEXDc; 1.
SMART; SM00359; DSRM; 1.
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Pfam; PF00271; helicase_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning and characterization of a novel human gene (HERNA) which encodes a putative RNA-helicase.", Blochim. Biophys. Acta 1490:163-169(2600).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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| ECENCE FROM N.A.
| MEDLINE=20246304: PubMed=10786632;
| Matsuda S., Ichigotani Y., Okuda T., Irimura T., Nakatsugawa S.,
| Matsuda S., Ichigotani Y., Okuda T., Irimura T., Nakatsugawa S.,
| Hamaquchi M.;
| Hamaquchi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DICE_HUMAN STANDARD: PRT; 1912 AA.
090BY3: 095943: 090002;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endoribonuclease Dicer (EC 3.1.26,-) (Helicase with RNase motif)
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ATP (POTENTIAL).
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RNASE III
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DICERI OR DICER OR HERNA OR KIAA0928
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MEDLINE*99246063; PubMed-10231032;
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Best Local Similarity
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PSD0517: RNASE_3_1; 1.
PS50142: RNASE_3_2; 2.
• ATP-binding: RNA-binding: Hydrolase; Nuclease; Endonuclease;
                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE HELICASE FAMILY.
SIMILARITY: Contains 2 Nease III domains.
SIMILARITY: Contains : PAZ domain.
SIMILARITY: Contains : DRBM (double-stranded RNA-binding) domain.
Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Chara G., Nagase T.;
           "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones.";
DNA Res. 9:99-106(2002).
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                                                                                                      Provost P., Samuelsson B., Radmark D.:
"Interaction of 5-lipoxygenase with cellular proteins.";
Proc. Natl. Acad. Sci. U.S.A. 96:1881-1885(1999).
-:- FUNCTION: Involved in cleaving double-stranded RNA in the RNA interference (RNA) pathway. It produces 21 to 23 bp dsRNAs (sirNAs) which target the selective destruction of homologous
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996399DB4B074F21 CRC64;
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KQ -> NT (IN REF. 1).
D -> H (IN REF. 1).
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EMBL: A.132261; CAB38857.2; ---
EMBL: A.5623145; BAA76772.2; ALT_INIT.
Genew: HGNC.17098; DICER1; ALT_INIT.
MIM: 606241; ---
                                                                                            MEDLINE-99162526; PubMed=10051563;
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Pfam: PF0071; het.loase_C: 1.
Pfam: PF00170; PAS: 1.
Pfam: PF00656; Riboniciease_3; 2.
SMARF: SM00487; DEXDG: 1.
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DUF283.
Helicase_C.
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Interpro: IPR001159; DS.RBG.
Interpro: IPR001594; DVP283.
Interpro: IPR001504; DVP283.
Interpro: IPR00160999; RAI.case.:
Interpro: IPR00160999; RAISE_3.
Pfam: PFC00370; DEAD: I.
Pfam: PFC0035; dSrm: I.
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SMART; SM00388; DSRM; 1.
SMART; SM00490; HELICC; 1.
SMART; SM00535; R1BCC; 2.
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS50821; PA7.
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ABO72102 Hepatitis
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ABO8091118 Cache Val
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AAC49101 Hepatitis
AC125317 Rattus no
AC127861 Rattus no
AF569258 Hepatitis
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AC006030 Homo sapi
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AC103315 Rattus no
AC09421 Rattus no
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AB01862 Hepatitis
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AB072067 Hepatitis
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AF070171
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-DATTS-BITE -STRAT-1 -RNP--1 -MATRIX-biosum62 -TRANS-Ancrach-Codi -LIST-45
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-DATTS-BITE -STRAT-1 -RNP--1 -MATRIX-BID-30-90-91 -NAXLEN-20-30-00-00-1
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-USRR-USS96594_GCN_1 13508_dcnat_29-92-00-1 140-2 -NCPU-6 -TOPU-3
-NORMAP -LARGEOUERY -NEG_SCARES-0 -WAIT -DSPECAR'-100 -NON-30-0
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                                                                                                                              September 30, 2663, 10:34:19 : Search Live 2262 Seconds (Without alignments) 167:296 Million cell updates/sec
               GenCore version 5.1.6
Copyright (c) 1993 · 2003 Compagen Ltd.
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Viruses: ssawA positive-strand viruses, no DNA stage: Flaviviridae;
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                                             Ogata,S.
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ATCVNGVCWTVFHGAGSKTLAGPKGP1TQMYTNVDQDLVGRPAPPGARSLTPCTGSS
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Submitted (26-SSP-2001) Satoshi Cqaid. Kobe Relycoshty, Graduate
School of Medicine. Department of Mirrohaclogy: 7-5-1 Kranneki-chen
Chuo-ku, Kobe. Hyego 550-2517, Japan
(E-mail:cqatas@med.kobe.d.ac.)p. Tolis1 28-42-5501,
Fax:81-78-382-5519)
               AB072047 540 bp RNA linear VFL 02-AFR-2002
Hepatitis C virus type 1b gene for polyprotein, NS3 region, partial
                                                                                                                    Viruses, ssRNA positive-strand viruses, no DNA stade: Flaviviridaes 
Repablyfins.
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CORREDATION BETWEEN SECONDARY STRUCTURE OF AN AMINO-TERMINAL
PORTION OF THE MONSTRUCTURAL PROTEIN 3 OF HEPATITIS C VIRUS AND
DEVRIOPMENT OF HEPATOCELLUTAR CARCINOMA
                                                                                                                                                                                                                                                                                                                                                                               /organism"Hepatitis C virus type lb"
/mol_type="genomic RNA"
/isolate="H05-4"
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/product="monstructural protein"
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/db_xref-"GI:19911839"
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Hepatitis C virus type 1b
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Chases 1 to 540)
Ogata,S.
Direct Submission
Sincer Submission
Submitted (26.55P-2001) Satoshi Ogata. Kobe University, Graduate
Submitted (26.55P-2001) Satoshi Ogata. Kobe University, Graduate
Submitted (26.55P-2001)
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Fax:81-78-382-55C1,
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atcingvcwtythgagskilagpkgpitqmyinvdldlvskgappgarsmtrctgss
dlylvtrhadvipvrrrgdgrgsllsprpvsylkgssggpllcpsghavgvfraavci
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Hepatitis C virus type 1b
Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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CÓRRELATION BETWEEN SECONDARY STRUCTURE OF AN AMINO-TERMINAL PORTION OF THE NONSTRUCTURAL PROTEIN 3 OF HEPATITIS C VIRUS AND DEVELOPMENT OF HEPATOCELLULAR CARCINOMA
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/mol_type="denomic RNA"
/isolate="HO5-5"
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Submitted (07-AUG-2002) Hak Hotta, Kobe University Graduate School
Submitted (07-AUG-2002) Hak Hotta, Kobe University Graduate School
of Medicinc, Division of Microbiology; Chuo-ku, Kusunoki-cho 7-5-1,
Kobe, Hyogo 659-0617, Japan (F-mall:hotta%kobe-u.ac.jp,
Tel:81-78-382-5500, Pas.81-78-382-5519)
Location/Qualifiers
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/isolate-"82"
/ib_xref-"taxon:31647"
/i.540
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Mismatches:
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175 c 167 q 102 t
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AB089533.1 G1:29467273
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Hotta,H.
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Hepatitis C virus type 1b gene for polypropola. NSA region, partial
Ab072102
                                                                                                                                                                                                                                                                                                                                                           /product-'polyprotein'
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RGVAKAVDFTPVESMETTMR"
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Submitted (26-SSP-2001) Satoshi Ogata, Kobe University, Graduate
School of Medicine, Department of Microbiology, 7-5-; Kusuncki-cho,
Chro-ku, Kobe, Hyogo 650-0017, Japan
(Ermail:oqatas@med.kobe-u.ac.jp, Tei:81-78-382-5501,
Fax:81-78-382-5519)
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sepatitis C virus type 1b
Viruses; SSRNA positive-strand viruses, nc DNA stage; Flaviviridae:
Hepativirus.
  Ogata,5.

Direct Submission

Submitted (25-SEP-2001) Satoshi Ogata, Kobe University, Graduate Submitted (25-SEP-2001) Satoshi Ogata, Kobe University, Graduate School of Medicine, Department of Microbiclogy, 7-5-1 Kusuncki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
(E-mail:ogatas@med.kobe-u.ac.jp, Tel:81-78-382-5501, Fax:81-78-382-5519)
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CORRELATION BETWEEN SECONDARY STRUCTURE OF AN AMINO-TERMINAL CORRELATION OF THE NONSTRUCTURAL PROTEIN 3 OF HEFATITIS 3 VIRUS AND DEVELOPMENT OF HEFATOCELLULAR CARCINGMA Uppublished
                                                                                                                                                                                  /organism="Hepatitis C virus type ib"
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Mismatches:
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37 CTACTTGGCTGCATTGTCACCAGCTT 63
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A 157 q 121 t
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Submitted (07-AUG-2062) Hax Hotta, Kobo University Staduale School
of Medicine, Division of Microbiology; Chuo-ku, Kusunoki-cho 7-5-1,
Kobe, Hyogo 650-017, Capan (E-mail:hotta@kobe-u.ac.jp,
Tel:81-78-382-5500, Fux:81-78-382-5519)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identification of Hepatitis C Virus (HCV) Subtype 1b Strains That Are Highly, or Only Weakly, Associated with Hepatocellular Carcinoma on the Basis of Secondary Structure of an Amino-Terminal Unpublished
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37 CTACTTGGGTGTATGGTCACTAGGGTC 63
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Hotta,H.
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BLYLTRHADVIPVRRRSDGRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCT
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Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Submitted (07-AUG-2002) Hak Hotta, Kobe University Graduate School
Submitted (07-AUG-2002) Hak Hotta, Kobe University Graduate School
Submitted (07-AUG-2002) Japan (E-mail: Hotta@kobe-u.ac.jp,
Cobe, Hyogo 650-0617, Japan (E-mail: Hotta@kobe-u.ac.jp,
Tel:81-78-382-5500, Fax:81-78-382-5519)
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                  Matches:
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                                                                                                                                                                                             /organism="Hepatitis C '/organism="Tepatitis C '/moi_type="genomic RNA" /isolate="Y-063"
                                                                                                                                                                       i LeuLeuGlyCysllelleThrSorLeu 9
                                                                                                                                                                                                                                                                                              24 C Pb
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/note="subtype: 1b"
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Hotta, H.
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DEFINITION

AB100809

LOCUS

RESULT

ACCESSION

VERSICN KEYWORDS

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

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/product-"polyprotein"
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//protein_id="BAG675371.1"
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DLYLVTRHADVJPVRHGDGSRGSLLSPRPVSYLKGSSGGPELCPLGHVVGJFRAAVCT
KGVAKAVDFVPVESMETTMR"
Hepatitis C virus
Hepatitis C virus
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bp RNA linear VRL 31-APR-2002
polyprotein gene, partial cds.
                                                                                                                                                                                                                                                   Direct Submission
Submitted (24-JAN 2003) Hak Hotta, Kobe University Graduate Schoo.
of Medicine, Division of Microbiology, Chuo-ku, Kusu:oki-cho 7-5-1,
Kobe, Hyogo 650-0017, Japan (E-mail:fotta@kobe-u.ac.jp,
Tel:81-78-382-5500, Fax:81-78-382-5519)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; sskNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                            Ogata.S. and Hotta.H. Indentitis C Virus (HCV) Subtype 1b Strains That Identification of Hepatitis C Virus (HCV) Subtype 1b Strains Ihat Re Highly, or Only Weakly, Associated with Hepatocollular Carcinoma on the Basis of Secondary Structure of an Amino-Terminal Portion of the HCV NS3 Protein
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J. Virol. 76 (8), 4034-4043 (2002)
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                                                                                                                                                                                                                                                                                                                                                                 1.540
/organism="Hepatitis C virus"
/mol_type="qenomic RNA"
/isolatc="qenomic RNA"
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/note="subtype: 1b"
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Hepatitis C virus
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Best Local Similarity:
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Hotta,H.
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AUTHORS
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AB100827.1 GI:29467692
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/db_xret-"g1:29467657
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ATCINGVCWTVYHGAGSKTLAGFRGPTIQNTTNVDJLVGNGAFPGASSMFPCTGGSS
BLYLVTRHADVIPVRREGDGRGSLJSPRPVSYLKGSSNGGFLJGPSGHANGIFFAAAVCTT
LSC 156 9 110 1
                                                                                ABIGO809 540 bp RNA linear VRL 02-APR-2003
Hepatitis C virus NS3 gene for polyprotein, partial eds, isolate:
Y-CH-06-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (24-JAN-2003) Hak Hotta, Kobe University Graduate School
of Medicine, Division of Microbiology, Chuc-ku, Kusuncki-cho 7-5-1,
Kobe, Hyogo 500-0017, Japan (E-mail:Hotta@kobe-u.ac.jp.
Tel:81-78-382-5500, Fax.81-78-382-5519)
                                                                                                                                                                                                                 Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                           Ogata,S. and Hotta,H. Indeptitis C Virus (HCV) Subtype 1b Strains That Identification of Hepatitis C Virus (HCV) Subtype 1b Strains That English, or Only Weakly, Associated with Repatocellular Carcinoma on the Basis of Secondary Structure of an Amino-Terminal Portion of the HCV NS3 Protein
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus"
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/mol_type="genomic RNA"
/isolate="Y-CH-06-R"
/db_xref="taxon:11163"
/note="subtype: lb"
i. 540
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                                                                                                                                                                          AB100809.1 GI:29467656
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/gene="NS3"
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2 (bases 1 to 540)
Hotta, H.
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Sest Local Similarity:
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FEATURES

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Query Match:

Fred. No.:

Score:

BASE CCUNT

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RESULT 9 AB100827

õ q ACCESSION

KEYWORDS

VERSION

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/specific_host = "Anopheles quadrimaculatus"
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Bost Local Similarity:
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TITLE
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MEDLINE
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                                                                                                                                                                                                                    /codon_start.3
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                                                                                                                                                                                                                                                                                              SENGITCETIFFIAAWHIKGRAVYLATYSSIGLASES.LLLAIROOGAALATTEEGGA
ALLLIAVISVITISPAYKILCKSKAWKSELIVKARAKIGEWPPRIGARGGGROFIWA
AVILLOTEUVPOTYMALAVIGPGHIRRSVESVPRYPAGALIKICAAVRESGGKY
CAMILIIGKWEGTYTYHHITPLOGWAHAGIRSIAVAVEPVVESSDHEKKIIKGARTAA
COOTIIGALPVSARKGRETIIGPADSIESGGWRILARITAYSGCTSGILGITYSELIGR
DRNOVERGROVYSTATGSFLATCVNGVCWTVYBGAGSKTLAGFKGFIJOMYINVDGGL
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Brockus,C.L. and Grimstad,P.R.
Comparative analysis of G1 glycoprotein-coding sequences of Cache
Valley virus (Bunyaviridae: Bunyavirus) isolates
Virus Senes 22 (2), 133-139 (2001)
             Direct Submission
Submitted (12-DEC-2001) Virology, Swedish Institute for Infectious
Disease Control, Solna SE 171 82, Sweden
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 2691);
Brockus,C.i., and Grims.ad,P.R.
Direct Submission
Submitted (17-SEP-1999) Vector Biology Laws, University of Notro-
Dame, Galyin Life Sciences Center, Notre Dame, IN 46556, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2691)
Brockus,C.L., Collins,F.H., Bosansky,N.L. and Grimstad,P.R.
Phylogenetic Analysis of Cache Valley Virus Isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA negative-strand viruses; Bunyaviridae; Orthobunyavirus; Bunyamwera virus group.
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AF187824.1 G1:6959495
   Kalinina, C., Norder, H., Mukemolov, S. and Magnius, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mote-"contains E2, p7, NS2 and NS3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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/mol_type="genomic RNA"
                                                                                                   /organisr="Hepatitis C virus"
/mol_type="qenomic RNA"
/strain="687"
                                                                                                                                                                                                                                                                                                                                                                                                                     279 t
                                                                                                                                                  /db_xref="taxon:11163"
/note="recombinant_2k/15"
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(bases i to 2691)
Brockus,C.L. and Grimstad, P.R.
Rockus,C.L. and Grimstad, P.R.
Comparative analysis of GI glycoprotein-coding sequences of Cache Valley virus (Bunyaviridae: Hunyavirus) isolates
Virus Genes 22 (2), 133-139 (2001)
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Brockus.C.L. and Grimstad, P.R.
Direct Submission
Submitted (04-PES-2000) Biological Sciences, University of Notre
Dame, Galvin Life Sciences Bldg. Notre Dame, IN 46556, USA
Location/Qualitiers
1. 2691
                                                                                                                                                        <1. ,>2691
/note="envolope glycoprotein; putative soluble portion"
/db_xref="taxon:80935"
/country="USA: Dennisville, NJ"
/note="1982 isolate from Ae. so:licitans"
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/mol_type-"genomic DNA"
/isolate-"Ar78-5912"
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/db_xref="G1:6959496"
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/product-"G1"
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SVGYNVOSKDNPFLLIDHYFTNRTYFHYDIGHTGIPTOGPHYN
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PADNHETLEVAHTKHIJGELOFKIMLGOJRYKSPASSPELEIDAKCVCCPSGFSYS
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ILMLFYIIENAFPGTTESLEYQLIQKRWTTGASKVLSKLITKYGNNNMFYGWWKGYG
LLTLPY TWTELSQNRRLIATQELESRHGGROESMSNAIQKSITKFCHNAKGYC
ISPREQIPIGKLIAGGOSPWYKTYKTFEKLYKNNKGEYWCSNCYCLAFDFERDEEV
VNKIKKLTCFLIDVSVEVDIFSVAASTCKNADKGKTVNGAKWNIKCBGGIYYFTDH
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                                                                            /product="Gl envelope glycopioleis"
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Cache Valley virus
Viruses: ssRNA negative-strand viruses: Bunyaviridae;
Viruses: ssRNA negative-strand viruses: Bunyaviridae;
Viruses: 1 to 2691)
Brockus,C.L. and Grimstad,P.R.
Brockus,C.L. and Grimstad,P.R.
Oroparative analysis of G1 91ycopronein-coding sequences of Cache
Valley virus (Bunyaviridae: Bunyavirus) isolates
Virus Genes 22 (2), 133-139 (2001)
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Brockus, C.L. and Grimstad.P.R.
Direct Submission
Submitted (04-FEB-2002) Biological Sciences, University of Notro-
Dame, Galvin Life Sciences Bldg, Notre Dame, IN 46556, USA
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/db_xref="taxon:80935"
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/isolate="61D240"
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                    /country-"USA: Ohio, Kent?
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/db_xre1-"taxon:80935"
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LIJEPYTNYTELSQNRKQTILATQESLSRSHSGRQSRGSBNSASATGGSVTRECHNARDYG
LSPREGIPIQHLTAGCOSPUYKIYKSNKGESNSWHCHNDFEBALBED
VNKVKLICFLTDVSVKTDIFSVAASTCKMADGGVCTVNDAKMNIKCDSGLYYFTDH
REGODTGONDFOEDYCISHFYFINFDILKCTWFFHSKRYTSTTSESLEFR
RAMTEKLSHILTIYNFKFHSANPHIRTYKFITANGVENSDGIESAYILSSIPALGG
SVGYNVOTKOMPPLILYDIVFKFRANJALFYKFITANGVENSDGIESAYILSSIPALGG
SVGYNVOTKOMPPLILYDIVFKFRONJERTYTYTHYDTGFTIGINYQHDEGCTGOPAV
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Cache Valley virus strait MI80-1-450 M segment, complete seguence.
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Virus Genes 22 (2), 133-139 (2001)
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Brockus, C.L. and Grimstad, P.R.
Brockus, C.L. and Grimstad, P.R.
Submission (14-SEP-1999) Vector Biology Labs, University of Notre
Dame, Galvin Life Sciences Center, Notro Dame, in 46556, USA
Location/Qualifiers
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Brockus, C.L., Collins, P.H., Besansky, N.L. and Grimstad, P.R.
Phylogenetic analysis of Cache Valley virus isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ache Valley virus
(ruses; ssRNA negative-strand viruses; Bunyaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLETTIDKNDKIEVNIGDQTSYIYEKDSRCKTWLCRVRDEG"
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/mol_type="genomic RNA"
/strain="M180-1-450"
/db_xref="taxon:80935"
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Indels:
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Brockus,C.L. and Grimstad,P.R.
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Fanning, L.J., Itakura, C., Nagayama, K. and Enomoto, N. Characteristics of Hepatitis C viral genome associated with disease progression in a homogeneous patient population
                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-oct-2000) Medicine, National University of Ireland, Cork, Hepatitis C Unit, Clinical Sciences Building, Cork University Hospital, Cork, Ireland
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SRPSWGPTDPRRKSRNLGKVIDILICGFADLMGYIPLYGAPLGGAARALAHGVRVLED
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AHTTRGLATLIFSFGPSQNI QLINTNGSWHI NRTALNCNDSLNTGFLAALFYAHRFNAS
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FTPSPVVVGTTDRFGVPTYSWGENETDVLLLNNTRPPRGNWFGCTWMNGTGFTKTCGG
PPCDIGGVGNDTLICPIDCFRKHPEATYTKCGSGPWLTPRCMVDYPYRLWHYPCTVNF
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LLLALPPRAYAMDREMAASCGGAVFIGLAIJITLSPHYKVFIARIJWHLQYFITRREAH
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AHGLIRACVI.VREVAGGHYVQMALMRLAALTGIYVYDHLTPLRDWAHEGLRDLAVAVE
PVVFSDMETKIIIWGADTAACGDIILGLPVSARRGREILLGPADSLEGGGKRLLAPIT
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DSRGSLLSPRPVSYLKGSSGGPILCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETT
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GFGAYMSKAHGVDPNIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIILCDECHS
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AIPIETIKGGRHLIFCHSRKKCDELAAKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVA
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RTGIYRFVTPGERRSGMFDSSVLCECYDAGCAMYELTPAETSVRLRAYLNTPGLFVCQ
DHLEFWEGVFTGLTHIDAHFLSQTRQAGDNFPYLVAYQATVCARAQAPPPSWDQMMKC
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ALAAYCLTTGSVVIVGRIILSGKPAIVPDREVLYQQFDEMEECATHLPYIEQGMQIAE
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PAIASLMAFTASITSPLTTQHTLEFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSI
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GVWRGDGIMQTTCPCGAQIIGHVKNGSMRIVGPRTCSNIWHGTFPINAYITGPCTPSP
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YAPPCKPLLREEVTFQVGLNOYLVGSQLPCEPEPDVAVLTSMLTDPSHITAEAAKRRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism."Hepatitis C virus"
/mol_type="mRNA"
/do_xref="taxon:11103"
/dof="faxon:11103"
/note="isolated from source plasma identified as the single source of the latrogenic infection of Rhesus negative women in Ireland from May 1977-November 1978; exposure was through HCV lb contaminated anti-D immunoglobulin"

    (bases 1 to 9359)
    Fanning, L.J., Itakura, J., Nagayama, K. and Enomoto, N.

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/protein_id~"AAL55821.1"
/db_xref="G1:18027685"
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YNSKNUP YSBOLNILYT ENNAFOTTH BILFFOLLOKKIT GASVULGKKIT KYON
NMFVGWKEGOTIL IPPET IN THE SOME TILLAFCELLSRHSGROFSMAN, OCS
TKBCHRAKGVECLSPFFF FLOWEL TAGGESPNYK I WITTEKLYKSNIKGEWENSNOW
CLOBGERVAK I KKLOTLOFLOVSFEV JESVAKIT CKRADSWYTHVANKWNI
KCDSGLYYFTHREGOTGOTGONFOLISHGNY FRIP I I DEDITKTIT CTWEETING SYT
STISSLESLESPKRAMARK KKLSHTLINNYK I TANJH I RETITKTIT CTWEETING SYT
                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="Aap3315.1"
/db_xref="G1:6959490"
/db_xref="G1:6959490"
/translation="MirbleInAriorsyning rathorhoghilaeskerisisesclix
bbysmlksbuvo="MirbleInAriorsyning rathorhophilaesh rathorhold rathorhophilaesh 
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EASDRMEIHEBSGLOGOYKSLIARLICKSKOSSLVISGLLSKLILSFYTPHGTTS
YPESRXYTLEBLIDWYRGLYSBONIKEYIVYSLFOSELLLGAFINSTILSKTTSTL
YRENYIYCEECSMYHSKREYNGFOTOROPTSTGLYTHWSTRYSTL
LKWARYLMILLYLLIAGHTLINGAFTNGGFOTOSOFOTOSPHLOGSCTNRYRS
DAEAQKLVSOSKISQLDADQVSLGNSIDSATKAIRAGKTYFTWHLLETHINKNUTSY
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DEHCTGPCPAVVPHKENWMIFSCERTSRWGCEEFGCLAINTGCVFGSGQDJTHPHIKV
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SCKLLKBETSLIFADNHETLEVAHTKHLIGBLOFKIMLGDIRYKSFAESPHLEIDAKG
VGCPSGFESYSGNFQIVTNIDTVGSVEGPCTLFHNRIITSANKOSYGLKKSGOTKFWQ
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EPLKAFFEGSYFSIIFYVVVGIIVLFLIIYIFLDMFFKLKDVLKRNEYLYIGGEIKHK
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Hepatitis
Hepatiti
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YLLSSIPALGGISVGYROVEDING, TRICKSAVLRITYNHIVEDTGT
YLLSSIPALGGISVGYROVEDING, WITTERFRYDGSCODI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus polyprotein mRNA, partial ods. AF313916
/country-"USA: Cass county, Michigan"
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Mismatches:
Indels:
                                                               /note="1981 isolate from equid"
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756 c 869 g 1288 t
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Matches:
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                                                                                                                                                                            "signal sequence"
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                                                                                                                                                                                                                                                                                                                                        /codon_start+1
/product-"polyprotein"
                                                                                                                                                                                                                                                                                          /note="G2-M-G1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="NSE"
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LOCUS
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TCYBKASAACRAAKLQDCIMLUVGDDLVVICESAVIXEDAASLAVFTEANIRYSAPEG DPRKPEYDLELITSCSSNVSVAHDASGKRVYYLTREPTTPLARAAMETARHTPVNSKL GNITWAPTBARMILMTHFFSILLACFGLEKALDCOLYGACYS. PERDZEOLIGACH GLSAFSLASYSPGETNRVAACLEKLUVPPLAVWHRKASVRAKLLSGGSRAANCGYT FLWAVRTKHTPIPAASGLDLSSWFVAGYSGGETYHSELSKARPKWFMLCLLLSVGV GIYLLDNR\*

283C C 2680 G 1968 L 4 olders

1877

BASE COUNT ORIGIN

9559 1000 000 Tength: Matches: Conservative: Mismatches: Indels: Gaps: 76 43.00 100.008 88.898 97.738 Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Dest Local Similarity:
Ouery Match:

US-09-965-594-1\_COPY\_14\_22 (1-9) x AF313916 (1-9359)

ò a Search completed: September 30, 2003, 12:51:59 Job time: 2207 secs

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17-JAN-1995
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-MODEL-frame-Lp2n.model -DEV-X1h
-MODEL-frame-Lp2n.model -DEV-X1h
-MODEL-frame-Lp2n.model -DEV-X1h
-MODEL-JJ/USPIO_SPOOJ/US09965594/runat_25092063_154249_14664/app_query.fasta_1.199
-DB-M_Geneseq_190un03 -OPMT-fastap -SUFFIX*rng -MINNATCH-0.1 -LOOPCH-0
-LOOPEXT-0 -UNITS*bits -START-1 -SND--1 -MATRIX*blosum62 -TRNS*human40.ndi
-LIST-45 -DOCALIGN-200 -THR_SCORE_EPCT -THR_MAX-99.9 -THR_MINN.0 -ALIGN-15
-USER-US0965594_6CGN_1 1312_erunat_29092003_164247_14064 -NCPU-6 -1CPU-3
-NO_MARP -LARGEQUERY -NGG_SCORES.0 -WAIT -DSPENCK=100 -LONSLOG
-FORVERY -LOOPERY -NGG_SCORES.0 -WAIT -DSPENCK=100 -LONSLOG
-FORVERY -LOOPERY -LOOPERY -SORES.0 -WAIT -DSPENCK=100 -LONSLOG
-FORPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELDENT=7
                                                                                                                               (Without alignments)
128.545 Million cell updatos/ser
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/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl983.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl983.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl983.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl983.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl983.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl983.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl988.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl988.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl988.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl988.Nal;
/SIBSI/gogdata/geneseqy/geneseqn-erbi/NAl989.Nal;
/SIBSI/gogdata/geneseqy/geneseqn-erbi/NAl989.Nal;
/SIBSI/gogdata/geneseqy/geneseqn-erbi/NAl989.Nal;
/SIBSI/gogdata/geneseqy/geneseqn-erbi/NAl989.Nal;
/SIBSI/gogdata/geneseqy/geneseqn-erbi/NAl969.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl962.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl962.Nal;
/SIBSI/gogdata/geneseq/geneseqn-erbi/NAl962.Nal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/gcnescq/genescqn-embl/NA1994_DAT:*/SIDS1/gcgdata/genescq/acmescqn-embl/NA1995_DAT:*/SIDS1/gcgdata/genescq/acmescqn-embl/NA1995_DAT:*/SIDS1/gcgdata/genescqqacmecqn-embl/NA1997_DAT:*/SIDS1/gcgdata/genescqq
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                                                                                                           : Search time 189 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                             5105271
Gendore version 5.1.6
Copyright (c) 1993 - 2003 - Compagne 1845.

    nucleic search, using trame_plus_p2n model

                                                                                                                                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                      2552756 segs, 1349719017 residues
                                                                                                           September 29, 2003, 19:09:03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 99%
Listing first 45 summaries
                                                                                                                                                                                 ns-09-965-594-1_COPY_14_22
                                                                                                                                                                                                                                                                             Xgapext
Ygapext
Fgapext
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length: 2000000000
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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BAC containing rep
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Arabidopsis thalia
Arabidopsis thalia
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DNA encoding novel
DNA encoding novel
Infectious hepatit
Nucleotide sequenc
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Plasmid pEI-BS(+)/
Borrelia burgdorfe
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HCV NS3 DNA. Hepa
CDNA encoding huma
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Rat calcium/calmod
Human hepatitis C
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                                                                                                                                                                        Non-A, non-B hepat
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                                                                                                                                                    NANBH virus qene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV NS4A-NS3
HCV N
                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
derived by analysis of the total score distribution
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                                     SUMMARIES
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AAF22305
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AAF23492
AAF22302
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AAC45995
AAC41345
AAC41345
AAC42388
AAC80326
AAC80326
AAC80328
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AAX80334
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AAS86668
AAS88891
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AAF22287
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AAS19166
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AAX20248
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AAX80317
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AAX24843
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AAX80305
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AAX80312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blood transmiscible NANBHV genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-B hepatitis virus.
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Query
Match Length DB
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1082138
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AAU64058;
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                                                            carrier
                                                                                                                                                                                                                                 Clery Match
                                                                                                                                                                                                                                                                                                                                   AA064068
                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                     This sequence represents the genome of a blood gransmissible non-A, non-B hepatitis (NANBH) virus. This sequence was isolated using the primers given in AAQ6580-35. The ambilited irraments are used in the detection of hepatitis virus. This target DNA was isolated from serum of chronically infected NANBH patients who were CLOC antibody-positive and EVO RNA (NSS region) positive. Reverse transcription-POR and PCR wore performed on CDNA and the total human NANBH DNA was constructed from 23 closes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen; structural; non-structural; non A non B hepatitis virus; NANBHV; NANBH; patient; plasma; diagnosis; detection; carrier; ss.
                                                                                                                                                           Blood-transmissible non-A non-P hepatitis virus DNA - used for detection of hepatitis virus % \left( \frac{1}{2}\right) =0
                                                                                                                                                                                                                                                                                                   Sequence 9436 BP; 1876 A: 2840 C: 2655 G; 1974 T: 91 otter:
                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-965-594-1_COPY_14_22 (1-9) x AAQ63499 (1-9436)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KOKU-) KCKUSAI SHIYAKU KK.
(SANW ) SANWA KAGAKU KENKYUSHO CU.
(TOFU ) TONEN CORP.
(TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHC.
                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuLeuGlyCysllelleThrSerLew 9
                                                                                                                                                                                        Claim 1; Page 8-20; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ58817 standard; cDNA; 819 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NANBH virus gene fragment #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92JP-0207391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93JP-0156087
                                                                                                                                                                                                                                                                                                                                653
43.00
100.00%
88.89%
97.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non A Non B hepatitis virus
                                                                     92JP-0051885
                                                                                       92JP-0051885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
342..9374
           /*:ag=
                                                                                                                               WPI; 1994~163130/20.
                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                            (KAEN/) KAENNO K.
                                                                                                                                         P-PSDB; AAR53417.
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                                                                                        10-MAR-1992;
                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                             JP06105690-A
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The sequences given in AAGSE814-27 encode antigens of structural and non-structural regions of non A non B hepatitis virus (NAMBHV). These sequences were derived from the plasma of a NAMBH patient by recombinant DNA techniques. These fragments are useful for the diagnosis of NANBH patients and the detection of NANBHV carriers.
                                                          Nucieic acid fragment coding non-A non-B hepatitis virus antigen - useful in diagnosis of NANB patient and detection of virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-A, non-B hepatitis virus; NANBHV; hepatitis C virus; HCV; core; ENV; NSI; NS2; NS3; antigen; detection; SS.
                                                                                                                                                                                                                                                                                                                                                     57
8 8 F O O O
                                                                                                                                                                                                                                                                                             other
                                                                                                                                                                                                                                                                                                                                                                                          Conscrvative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                             Sequence 819 HP; 150 A; 255 C; 241 G; 173 T; 0
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                                                                                                                                                                                                                                                                                                                                                                            Matches:
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/note= "NS3 N-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-A, non-B hepatitis virus gene #4
                                                                                                                                   Claim 8: Page 18-19: 37pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SANW ) SANWA KAGAKU KENKYUSHO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
307..879
/*tag= b
/label= core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ64068 standard: cDNA: 3461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          880..1455
/*tag= c
/label= ENV
1456..2736
/*tag= d
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42.66
100.60%
68.89%
95.45%
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WPI; 1994-128677/16
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                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Bost Local Similarity:
                      P-PSDB; AAR50072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP06141870-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1992;
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                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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AAS86658;
                                                                                                                                          Query Match:
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                                                                                                                                                                                                             AAS86668/c
                                                                                                               Fred. No.:
                                                                                                                                                                                                       RESULT 5
 ć
                                                                                                                                                                                                                            DNA coding a Non-A, non-B hepatitis virus antigen - useiu; for detecting HCV within serum
                                                                           Hepatitis C virus 44 and #6 genes were isolated (AAQ64068-69).
Both genes contain the core, ENV, NSI, NS2 and NS3 regions.
A core region fragment is given in AAQ64067.
                                                                                                                                                                                                                                                                                         Hepatitis C virus, HCV; antigen; detection: antibody; ds.
                                                                                                       Sequence 3461 BP; 638 A; 1046 C; 1012 G; 765 T; 0 other;
                                                                                                                           3461
8
1
0
0
                                                                                                                                          Conservative:
                                                                                                                                                                          US-09-965-594-1_COPY_14_22 (1-9) x AA064068 (1-3461)
       (TOKR-) 2H TOKYOTO RINSHE IGAKU SOGO KENKYUSHA.
                                                                                                                                                                                                                                                                          5'UTR/CORE/ENV/NS1/NS2/NS3 cDNA from HCV (#4).
                                                                                                                                                Mismatches:
Indels:
                                                                                                                            Length:
Matches:
                                                                                                                                                                                                1 LeukeuGiyCysilcileThrSerLeu 9
                                                                                                                                                                                                                                                                                                                                                /*tag= b
/product= Core peptide
880.1455
/*tag= c
                                                             Claim 1-5; Page 11-15; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                   /product= NS2 and NS3
                                                                                                                                                                                                                                                                                                                     Loration/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              /product - NS1/ENV2
2737. 3461
                                                                                                                                                                                                                                  AAT30386 standard: cDNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/product= ENV:
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                                                                                                                                 42.00
100.00%
88.99%
95.45%
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P-PSDB; AAR98361.
                    WPI: 1994-205026/25
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(TCFU ) TONEN CORP
                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                      Hepatitis c virus.
                           AAR54066
                                                                                                                                                                                                                                                                                                                                                                                                                                 JP07133291-A
                                                                                                                                                                                                                                                             22-AUG-1996
                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                      3421
                                                                                                                                                                                                                                              AAT30386;
                            P-PSDB;
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The invention relates to isolated polynucleotide (1) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques
                                                                                                                                                                                The sequences given in AAT30386-37 encode the 5'UTR/CORE/ENV/NS1/NS2/NS3 protein region derived from hepatitis C virus (HCV) isolates #4 and #6 respectively. The proteins encoded by these sequences particles encode amino acids 394-45 of the HCV NS1 antigen. These protein fragments may be used in the detection of antibodies against HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
Recombinant polypeptide comprising partial NSI region of hepatitis
non A non-B viral antigen - used in a method for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                             Seguence 3461 BP; 638 A; 1046 C; 1012 G; 765 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding movel human diagnostic protein #22472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CS-09-965-594-1_COPY_14_22 (1-9) x AAI30386 (1-3461)
                                                              antibodies against hepatitis nen-A non-B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
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                                                                                                                            Disclosure: Page 10-12; 15pp; Japanese.
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23-AUG-2000, 2000US-0649167.
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P-PSDB; ABG22481.
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Best Local Similarity:
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to restore normal activity of (II) or to treat disease states involving quantitating a polypetide in tissue, as melecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II) and (II) and its binding partners are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polymented responsible for genetic disorders or defection of mutations responsible for genetic disorders or defect traits to assess biodiversity and to produce other types of data and produces sees biodiversity and to produce other types of data and produces themso hid and ordered and sequences. AAS64197-AAS94564 represent movel human bote: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from Wipo
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                                                                                                                                                                                                                                                                                         Sequence 4977 BP: 1417 A: 1392 C: 1202 G: 966 T: 0 other;
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Conservative:
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AAS88891/c
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and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aborrant protein expression or biological activity. The polypeptide and polypurdleschide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197 AAS94564 represent nove; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
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Mismatches:
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polypoptide (II) sequences. (I) is useful as speridisation probes, and gene mapping, and in recombinant production of (II). The polymorace chain reaction (PRP) princes, oliquents, and in recombinant production of (II). The polymoracelides are also used in disatiostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for destreamoral activity of (II) at no treat, disease status incording quantitating a polypeptide in tissue, as molecular weight markers and us a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) are useful for treating discorders involving abeneating expression or biologica, setivity. The polypeptide and polynocleotide sequences have applications in
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Note: The sequence data for this pation, did not appear in the printed specification, but was obtained in electronic formst directly from WiPO
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 invention relates to isolated polynucleotide (1) and
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Mismatches:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-501.-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX24843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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the present sequence comprises the nucleic actd sequence of the geneme of infectious hepatitis C virus (HCV) genotype 1b strain Br.24 (HCV) genotype 1b strain transfected into cells. HC-14 was obtained from cutte phase plasma of a chimpance experimentally infected with serum containing of a chimpance experimentally infected with serum containing to produce chimpance factions nucleic acid sequence can be used to produce chimpance genomes (see AAX2483) consisting of the open reading frames of infectious nucleic acid sequences of other centypes (inciding senotypes 1-6) and subtypes (suciding senotypes 1-6) and sequence and the introduction of mutations or deletious nucleic acid sequence or also be used to produce attenuated virus via passage in vitro or in the intertious nucleic acid sequence. Waccines comprising one or more polypeptides made from the infectious nucleic acid sequence or companies the virus. The nucleic acid sequences can also be used to inmunity adainst the virus. The nucleic acid sequences or their encoded proteases (e.g. NS3 protease) can additionally be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric virus; bovine viral diarrhoea virus; BVDV; hopatitis C virus;
HCV; vaccine; viral inhibitor; antiviral; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of a hepatitis C virus (HCV) close genotype 1b.
New isolated hepatitis C virus nucleic acids - used to develop products for the diagnosis, prevention and treatment of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 9595 BP; 1934 A; 2842 C; 2698 G; 2121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --೦೦
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
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                                         infections and for developing screening assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lengt.h:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualitiers
342..9374
                                                                               Claim 3; Fig 14A-F; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA086939 standard; DNA: 9595 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.66e+03
41.00
100.00%
88.89%
93.18%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repatitis C virus.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W0200075352-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
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Score:
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                                                                 New nucleic acid comprising a chimeric boving viral diarrhose virus genome in which the (non-)structural region has been replaced by hepatitis C virus (HCV) genome useful for treating or preventing HCV
                                                                                                                                                                                                                                                                                                                                  Sequence 9595 BP; 1934 A; 2842 C; 2698 G; 2121 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yanagi M. Emerson SU, Purcell RH;
                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GBV-B; hepatitis C virus; HCV; vaccine; ds
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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          Purcell RE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Infectious Hepatitis C virus 1b genetype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LeuLeuGlyCyslleIleThrSerLeu 9
                                                                                                                          Disclosure; Fig 4A-F; 97pp: English
          Emerson SIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF23492 standard: DNA; 9595
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41.00
100.00%
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93.18%
22
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                                WPI; 2001-071081/08
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                                                                                                    signs and symptoms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                            P-PSDB; AAB31170.
         Bukh J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200075337-A1.
                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
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The present invention relates to GB virus-B. The nucleic acid molecules of the invention are useful for indirectly studying the molecular properties of hepatitis C virus (HCV). The infectious nucleic acid sequence of the GB virus-B clone and the HCV/GBV-B chimeras may be used in the development of vaccines and therapeutics for HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transpenic plant and aminal cells expressing selected proteins such as hormones, enzymes, interieukins, clotting factors, cytokines, antibodies, and growth factors.
New infectious nucleic acids of the GB virus-B clone, useful for indirectly studying the molecular properties of hepatitis C virus (HCV) and in developing vaccines and therapeutics for HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells
                                                                                                                                                                                                                                                                                                         Sequence 9595 BP; 1934 A; 2845 C; 2697 G; 2121 T; 0 other;
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88 40
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LeuLeuGlyCysileIleThrScrteu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector; ds
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                                                                                                       Disclosure; Fig 7; 96pp; English.
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99US-0134770.
99US-0153584.
99US-0154603.
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41.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copenhaver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W0200055325-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF22302;
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Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells \,
                                                                                                                                                                                      BAC containing repeats from centromeres 1-4 #10.
                   44375 ITGITAGGIIGCATIGIAGAGGAGIAIG 44349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 102; Page 484-508; 1449pp; English.
    1 LeulouGlyCysIleIleThrSerLeu 9
                                                                                                                                                                                                                    Centromere, michrosome, vector, ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keith K;
                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF22286 standard; DNA; 134499
                                                                                             AAF22287 Standard; DNA; 103929
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99US-0127409.
99US-0134770.
99US-0153584.
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41.00
100.00%
77.78%
93.18%
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                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copenhaver G,
                                                                                                                                                                                                                                               Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-587529/55.
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                                                                                                                                                                                                                                                                             WC200055325-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                 18-KAY-1999;
13-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                    18-MAR-1999;
01-APR-1999;
                                                                                                                                                        20-MAR-2001
                                                                                                                                                                                                                                                                                                         21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preuss D,
                                                                                                                           AAF22287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct comprising a plant centromers, useful for producing stably inherited michrosomes which can serve as vectors fithe construction of transgenic plant and animal cells.
   CTHETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 94895 BP: 28943 A: 18101 C: 18466 G: 29385 T: 0 other;
18101 C: 18466 G; 29385 T: 0
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                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                    US-09-965-594-1_COPY_14_22 (1-9) x AAF22302 (1-94895)
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Conservative:
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Matches:
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                                                                                                                          Gaps:
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990S-0127409.
990S-0134770.
990S-0153584.
990S-0154603.
Sequence 94895 BP; 28943 A;
                                                       41.00
100.06%
77.78%
93.18%
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                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-587529/55.
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Best Local Similarity:
Query Match:
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18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-MAR-1999;
                                                                                                                                                                                                                                                                                                                                    20-MAR-2001
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Pred. No.:
                               Alignment Scores:
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AAF22302;

AAF22302/c

Ouery Match

Score:

Preuss D,

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The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transquire plant and animal cells expressing selected proteins such as hormones, enzymes, interfeukins, clotting factors, cytokines, autibodies, and growth factors.
                                                                                                                                                                                 Sequence 103929 BF: 32987 A; 19310 C; 18547 G; 33085 T; 0 other;
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7
2
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-965-594-1\_COPY\_14\_22 (1-9) x AAF22302 (1-94895)

Score:

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Search completed: September 29, 2003, 19:19:33
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  18-MAR-1999;
01-APR-1999;
18-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors in the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interfectains, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct comprising a plant centromere, useful for
producing stably inherited michrosomes which can serve as venters the
the construction of transgenic plant and animal cells.
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Mismatches:
Indels:
BAC containing repeats from centromeres 1-4 #9.
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                                                Centromere: michrosome; vector; ds
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99US-0127409.
99US-0134770.
99US-0153584.
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                                                                                           Arabidops:s thaliana
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01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
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Pred, No.:
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The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transposic plant and animal cells expressing selected proteins such as because, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for
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                                                                                                                                                                                                                                                                                                                                                                    the construction of transgenic plant and animal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-965-594-1_COPY_14_22 (1-9) x AAF22305 (1-1082138)
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Conservative:
Mismatches:
Indels:
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990S-C125219,
990S-C1274C9,
990S-C134770,
990S-C153584,
990S-C1546C3,
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GenCore version 5:1.6
Copyright (c) 1993 - 2003 Compagen Ltd.
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8 : Search Lind 1625 Seconds
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134.679 Million cel. updates/sec
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OM protein - nucleic search, using trame_plus_p2c model
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                                September 29, 2003, 19:11:08
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Perfect score:
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                                                                                                                                      Sequence:
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Minimum DB seq length: 0 Maximum DB scq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 99% Listing first 45 summaries

em\_gss\_rod:\*
em\_gss\_phg:\*
em\_gss\_vrl:\*
gb\_gssl:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_fu:.\* •:wmq\_ssp\_ma:• em\_gss\_v:t:\* em\_gss\_mam:\* ∗:snш\_ssb\_mə em\_gss\_pro: em\_estium:\* em\_esthum:\* em\_estro:\* em\_htc:\* gb\_est2:\* qb\_htc:\* em\_estin:\* em\_estba:\* em\_estov:\* em\_estpl:\* qb\_est3:\* qb\_est4:\* qb\_est5:\* qb\_est.1:\* 16: 17: 19: 20: Database

## 29: gb\_qss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ici		1427 AUI	1.950918 Arabido	52875 SALK_UR	352/2 Arabido	58372 SALK_UI	11538 274341	01037 274340	102 FZOHIIFB	11201 000	89143 SALK_U	TIPP GCCTE	9/4 FZ:D4TFC	11494 AULLEZ	Alles Autres	4:1:7 AUTIES	1591 AUILGS	41228 AUILDI	29018 PUHJVS	363288 PUHLI	F167496 601775	900243 ti76d09	AI587235 tq21104.x	583735 rr03h01	4902724 PCS0186	F109646 7166c06	F727441 by21ell	2759141 HS_2201	721993 zh17d1	33709 18779 INI 317004 ANDO-00	312004 Obsyeu8. 565172 hi87ail	327322 WORGELL	0017316 U1-H-DT	2785099 6014783	15452 ym29906.s	15273 ym30e09.s	4682281 UI-E-EJ	25209 ic50c11	84273 UI-E-EJ	87309 UI-E-EJ	85367 6026372	27696 AGENCOU
GI		:241	195091	7.35.287	7000	759078	.07007	001004	201068	000	γ., Υ.,	00.1	47.4	4 4 4 4	1116	1	155	1122	2901	5328	5749	2.5	AIS8/235	77.7	3272	1964	27	5914	200	200	٠. د د	132	1731	350	152	27	3228	25	3427	3730	3536	5769
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## ALIGNMENTS

RESULT 1
BH241427 C
LOGIS
BH241427
LOGIS
DEFINITION AULP55TR AUIL Arabidopsis thaliana genomic clone AUILF55, genomic survey sequence.
ACCESSION BH241427.1 G1:16915855
KEYWORS
KEYWORS
SOURCE
Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota: Viridiplanta, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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Percent Similarity
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COMMENT
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AUTHORS
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KEYWORDS
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Bukaryota, Viridplantae, Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnollophyta; eudicotyledons: core endicots;
rosids; eurosids II; Brassicales: Brassicacae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosso,M., Strizhov,N., Li.Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Rat) for fianking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-00T-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koelt, 50829, Germany This sequence is recovered from the left border of the T-DNA. It
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strizhov, N., Li, Y., Rosso, M., Vichoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="AUIL"
//note='vector: pHGS2; Site_l: BstX1: 2-3 kb sheared BACDNA inscrted into pHGS2 using BstX1 linkers"
19 c 8 g 35 t
                Town,C.D., Whitelaw,C.A., Pai,G., Va:: Aken,S.E., Utterback,T.V.,
Feldblyum,T.V. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
                                                    Survey sequencing of Arabidopsis thaliana BAC F25J21
Unpublished
                                                                                                                                         9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 106
0 0 0 0 0 0
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Li.Y., Rosso.M., Strizhov.N. and Weisshaar.B.
Direct Submission
                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
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/clone="AUILF55"
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                                                                                                                                                          Tel: 301-838-3523
Fax: 301-838-6208
Email: cdtcwn%tigr.org
From Wash. U contig 720.
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                                                                                       Other_GSSs: AUILF55TF
Contact: Chris Town
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/organism-"Arabidopsis thaliana"
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/strain-"columbia OF
/strain-"columbia OF
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/db_xref="ftaxon:3702"
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/clone="ish-"Arabidopsis thaliana T-DNA from Arabidopsis thaliana plants (TI) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA finsertions. The DNA fragment(s) resulting from the PCR wore directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalalian nuclear genome sequence were
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indicates an insertion within the locus defined by clone F4MLY. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz.co.on.iig.de/GABI-Kat/.
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Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota: Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicctyledons; core eudicots; rosids;
curosids II; Brassicales; Brassicaceae; Arabidopsis.

[ (bases 1 to 34)
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C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, F., Zimmerman, J. and Ecker, J. K.
A Sequence-Indexed Library of Inscrtion Mutations in the
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1. .424
/organism-"Arabidopsis thaliana"
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/clone-"sak.2018581.33.10.x"
/clone-"pcR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence the site of insertion. Details of the protocols used can be found a. http://signal.salk.edu/tdna_protocols.html"
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota: Viridiplantac, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota: Magnoliophyta; endicotyledons; core endicots; rosids
peurosids II: Brassicales; Brassicaceac, Arabidopsis.
I (bases I to 424)
Alonso, J.W., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab
C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
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Salk Institute Genomic Analysis Laboratory (SIGRAL)
The Salk Institute for Biological Studies
10010 M. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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BH758372.; GI:19043622
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Salamoubal,M., Choisne,N., Artiguenave,F., Brottier,P., Wincker,P., Urpublished
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                                               /db_xref="taxon:3702"
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/coloe="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna.protocols.html
a 71 c 60 g 51 t lothers
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BP 191-91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
- Web : www.genoscope.cns.fr)
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/note="end : T?"
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/organism-"Arabidopsis thallana'
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                                   /strain="Columbia 0"
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PCR PRimers
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Best Local Similarity;
Query Match;
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B96162/c
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                                                                                                                                                                                                                                                                                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.c. Vector identified by cross_match with the "minscore is
                                                                                                                      Smith, T.P.L., Grosso, W.K., Freking, B.A., Roberts, A.J., Stone, R.T., Saass, E., Wray, J.E., White, J., Cho, J., Pahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, R.W., Rohrer, G.A., Chitac-McKown, C.G., Pertea, G., Holt, L., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a quee index for cattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /close_lb="MARC 3BOV"
/close="Vector: pCMV SPORT6; Site_l: Not!; Site_2; Sall:
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendenceus muscle, and fetal
longissimus muscle,
3 96 c 115 g 117 t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi:
Mammalia; Eutheria; Cetartiodactyla; Ruminantia: Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                        Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                         Eukaryota; Metazoa; Chordata; Cramiata: Vertebrata: Euteleostemi;
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                                                                                                                                                                                                                                                                                                                                     USDA, ARS, US Meat Animal Research Center
PO Box :66, Clay Center, NF 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
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Matches:
Conservative:
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/organîsm="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCAGGGG
Plate: 63 row: B column: 22
Seq primer: ATTIAGGIGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNN"
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/tissue_type="pooled"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: AGGAAGAGGTATGACCAT
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PCR PRimers
BF651538.1 GI:11915668
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88.89%
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41.00
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                                     Bos taurus (cow)
Bos taurus
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1. .465
/organism="Bos taurus"
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/tissue_type="pooled"
/tissue_type="pooled"
/tissue_trom marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle.
21 a 97 c 122 g 125 t
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F26H1TFB IGF Arabidopsis thaliana genomic clone F26H1, genomic
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( doses 1 to 498)
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter
Smith.T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fabrenkrug, S.C., Bennett G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.S. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980954.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update {\bf 3}
                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL USDA, ARS, US Meat Animal Research Center Po Box 16¢, Clay Center, NE 68933-016¢, USA TT-1: 402 762 436¢ Fax: 402 762 436¢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
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Arabidopsis thaliana
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BACKWARD: GTTTGCCAGTGACGACG
Flate: 63 row: B column: 21
Seq prime: ATTTAGGGGGGACTATAG.
Location/Oualifiers
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B96162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B2289143 SALK_022540.51.60.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_022540.51.60.x, genomic
                                                                                          /clone_lib="TAMO"
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/cote="Vector: BelobACil; Site_l: Hindili: Site_2: Hindili
: Produced by Rod Wing"
a 107 c 93 q 131 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alonso. J. Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of TDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute Genomic Analysis Laboratory (SIGNAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolia, CA 92037, USA 1101: 858 458 458 400 x1752 Pax: 858 558 6379 Email: eckerésaik.edu
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Corganism="Arabidopsis thallama"
/mol type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                             Matches:
Conservative:
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Arabidopsis thaliana
                                                                                                                                                                                                                                           Length:
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                                                                              /sex="hermaphrodite"
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1. .651
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41.00
100.00%
77.78%
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B2289143
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ORGANISM
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ORIGIN
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                                                                                                                                                              SASE COUNT
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Arabidopsis thaliana
Bukaryota: Viridiplantae: Streptophyta: Erbryophyta: Trachechyta:
Spermatophyta: Magnollophyta: erdinosylodoms: core eudinots: rosids:
- enrosids II: Brassicales: Brassicaceae: Arabidopsis.
1 (bases 1 to 505)
Rounsley, S.D., Kelley, C.M., Field, C.E., Craven, M.B., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B26036 13-0CT-1997 TAMU Arabidopsis thaliana genomic clone 1562, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter, J.C.
Use of a BAC End Sequence Database To Identify Minimal Overlaps for
                                                                                                                                                                                                                                                                                                                                                                           /sex."hermaphrodite"
/clone_lib="IGF"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI:
Produced by Thomas Altmann"
            Other GSSs: F25H17k
Contact: Steve Rounsley
Department of Eukaryotic Genemics
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 G200
Fax: 361 838 G208
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Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, ML 20850, USA
Tel: 301 838 0200
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Matches:
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="F26H1"
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Location/Qualifiers
1. .498
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Seq primer: M13-21
Class: BAC ends
                                                                                                                                                        Email: rounsley&tigr.org
Seq primer: M13-21
Class: BAC ends
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Other_GSSs: T5G2TR
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B95974.1 G1:2998450
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 683)
Town,C.D., Whitelaw,C.A., Pal.G., Van Aken,S.E., Utterback,T.V., Feldbyum,T.V. and Fraser,C.M.
Unpublished
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DEFINITION F21D4TFC IGF Arabidopsis thaliana genemic clone F21D4, genomic
                                                                                                                                                                                                        AULE77TF AUL Arabidopsis thallara genomic clone AULE77, genomic surey sequence.
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/clone-"Adile77"
/clone_lib="Adil.e77"
/roter-lybercar: pHSZ: Site_l: HstXI; 2-3 kb sheared BAC /noter-voctor: pHSZ: Site_l: HstXI; 2-3 kb sheared BAC late pHGSZ using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockwille, Mp 20855, USA
           .ocation/Qualifiers
1 683
//organism="Arabidopsis thailana"
//moi_rype="genomic DNA"
/strain-"Columbia"
           Length:
Matches:
Conservative:
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Fax: 301-838-0208
Email: octown@tigr.crg
From Wash. J conlig 720.
Sog primer: TF
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COMMENT
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BH241556
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AUTHORS
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota: Majolantae, Streptophyta; Embryophyta: Tracheophyta;
Bukaryota: Viridiplantae, Streptophyta; Core eudicots; rosids
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; rosids
curosids II: Brassicales; Brassicaceae: Arabidopsis.
I (bases I to 719)
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; Core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases ito 693)
Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Adams, M.D. and Venter
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/clone_lib="IGF"
/note="Vector: BeloBACII: Site_1: EcoRI;
/note="Vector: BeloBACII: BeloBACII: Site_1: EcoRI;
/note="Vector: BeloBACII: BeloB
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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1. .693
Accoganism="Arabidopsis thaliana" Accol. Lype="qenomic DNA" Strain="Columbia"
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Seg primer: M13-21
Class: BAC ends
High quality sequence stop: 693.
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/clone="F21D4"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukanyota: Viridiplanea
Eukanyota: Viridiplanea
Streptophyta: Governophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; rosids
curosids II: Brassicales; Brassicanceae; Arabidopsis.
I (bases i to 78)
Town, C.D., Whitelaw, C.A., Pai, G., Van Aken, S.E., Utterback, T.V.,
Feldblyum, T.V. and Fraser, C.K.
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AULLF85TF AUL Arabidopsis thaliana genemic clone AULF85, genomic
/note-"Organ: Leaf: Vector: pHOSI; Total genomic DNA was sheared to 0.9-1 Khp before ligation."
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/mol_type="genomic DNA"
/strain="columbia"
/db_xref="axon:3702"
/clone="AUILF85"
/clone="Vector: pHOS2; Site_1: BstXI: 2-3 kb sheared BAC DNA inserted into pHOS2 using BstXI linkers"
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Tel: 301-838-3523
Fax: 301-838-3523
Fax: 301-838-352
From Wash. U contig 720.
Seg primer: TF
Class: sheared ends.
Location/Oualifiers
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Matches:
Conservative:
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BH241165
BH241165.1 GI:16915368
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Contact: Chris Town
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantac; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicoty;edoms; core cudionts; risids;
euroskids II; Brassicales; Brassicaceacac, Arabidopsis,
1 (bases I to 724)
Bueli, C. R., inc, X., Pai, C., Barnstead, M., Bowman, C., Ctterbach, T., Rabidopsis, Lang, F., Creasy, T., and Fraser, C.M.
Conomic survey sequencing of Landsberg enecta ecotypn of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A0955329 1500 724 bp DNA linear GSS 28-JAN-2000 LERAD34TF LERA Arabidopsis thaliana genomic clone LERAD34, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Xiaoying Lin
The Institute for Genemic Research
9712 Medical Center Dr., Rockwille, MC 20850, USA
Tel: 301-838-0206
Fax: 301-838-0208
Email: at&tion: Org
For additional information, see http://www.tigr.org/tdb/at/at.html
                                                                                                                                                                                                                           9712 Medical Center Drive, McGKV11bs, MD 20850, USA.
Tel: 301-838-5523
Fax: 301-838-0208
Email: odtowdigr.org
From Wash, U contig 720,
Seq primer: TR
Class: sheared ends.
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                                                                                                                                              Location/Qualifiers
1. 719
Coganism="Arabidopsis thaliana"
/mol type="Qenomic ENA"
/strain="Columbia"
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Matches:
Conservative:
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/mol_type="genomic DNA"
/strain="landsberg erecta"
/db_xref="taxon:3702"
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/clone_lib="LERA"
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AQ955329
AQ955329.1 GI:6783030
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41.00
10C.00%
77.78%
 Contact: Chris Town
Tick
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Class: shotgum.
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Unpublished
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88.9%; Pred. No. 1.1;
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01-JUN-2002 (TrEMBLrel. 21, Last sequenc
01-OCT-2002 (TrEMBLrel. 22, Last annotat
Polyprotein (Framment)
Hepatitis C virus type 1b.
Viruses: SSRNA positive-strand viruses, Hepativius.
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080W22
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09J3G4
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Matches 8; Conservative
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STRAIN-LOB;
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Q8gw28 hepatitis
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                                                                                                                                                                                          September 29, 2003, 19:00:07 : Search time % Seconds
(without aliquments)
77:416 Million cell updates/sec
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089w27 |
                          GenCore version 5.1.6 Copyright (c) 1993 \times 2003 Compugen 5td.
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090IY5
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Q8QW19
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4: sp_human:*
5: sp_invertebrate:*
6: sp_marmal:*
7: sp_mhor*
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sp_unclassified:*
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sp_bacteriap:*
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sp_phage:*
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Maximum Match 99%
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sp_bacteria:*
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sp_rodent:*
sp_virus:*
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Maximum DB seg length: 2000660000
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Match Length DB
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Score

Result . 9 

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Schartze 21964745; FubMedall 977242;

Kallrina O., Norder H., Mukomolov S., Machius L.O.;

Talatural interpresentation recombinant of hepatitis C virus identified in St. Petersburg.;

I. J. Virol. 76:4004403440202).

R. Titerpres IPR002531; HCV_NS2.

R. Titerpres IPR002531; HCV_NS2.

R. Titerpres IPR004109; HCV_NS3.

R. Pfam: PF01589; HCV_NS3.

R. Pfam: PF01589; HCV_NS3.

R. Pfam: PF01589; HCV_NS3.

R. Pfam: PF02507; HCV_NS3.

R. Pfam: PF02507; HCV_NS3.

R. Pfam: PF01589; HCV_NS3.

R. Pf01589; HCV_NS3
                                                                                                                                                                                                                                                                                                                                                                                               Ogata S.;
"CORRELATION BETWEEN SECONDARY STRUCTURE OF AN AMINO-TERMINAL PORTION
OF THE NONSTRUCTURAL PROTEIN 3 OF HEPATITIS C VIRUS AND DEVELOPMENT OF
HEPATOCELLULAR CARCINOMA.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AB072102; BANBS24.1;
Interpro: IPR004109; HCV_NS3.
Pfam: PF02907; HCV_NS3: 1.
GI-JUN-2002 (TrEMBLrel. 21, Created)
JOH-2002 (TrEMBLrel. 21, Last sequence update)
GI-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Polyprotein (Fragment).
Polyprotein (Fragment).
Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
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Viruses, ssRNA positive-strand viruses, no DNA stage, Flaviviridae,
Hepacivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.7%; Score 43; DB 12; Length 180; Best Local Similarity 88.9%; Pred. No. 1.1; Matches 8; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEQF94 PRELIMINARY; PRT; 403 AA. 0802P94; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUNAR-2003 (TrEMBLrel. 23, Last ancotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome polyprotein (Fragment).
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Best Local Similarity 88.9°
Matches 8; Conservative
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|3 LIGCIVISL 21
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                                                                                                                                                                                                                                                        NCBI_TaxID=31647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID-11103;
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                                                                                                                                                                                                                                                                                                                                                                 STRAIN-82;
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SEQUENCE
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Submitted (SEP-2061) to the EMBL/GenBank/DDRJ databases.

EMBL; AB072047; BAB88229.1; -...

InterPro; IPR04409; HCV_NS3.

Pfam; PF02907; HCV_NS3.

NON_IPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saps
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                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TreMBLrel. 22, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus type 1b.
Viruses; ssRNA positive-strand viruses, no ENA stade; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     080W27;
01-JUN-2002 (TrEMBLRel. 21, Croated)
01-JUN-2002 (TrEMBLRel. 21, Croated)
01-ONT-2002 (TrEMBLRel. 22, Last sequence update)
01-ONT-2002 (TrEMBLRel. 22, Last annotation update)
10-ONT-2002 (TrEMBLRel. 22, Last annotation update)
10-ONT-2002 (TrEMBLRel. 22, Last annotation update)
10-ONT-2002 (TrEMBLRel. 21, Last annotation update)
10-ONT-2002 (TrEMBLRel. 21, Castandal update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.7%; Score 43: DB 12: Longth 150; 88.9%; Fred, No. 1.1; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.7%; Score 43; DB 12; Length 180;
88.9%; Pred. No. 1.1;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AB072048; bas88230.1;
InterPro; IPROG4109; HCV_NS3.
InterPro; IPROG4109; HCV_NS3.
NON_TER
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Best Local Similarity 88.5.
Fram 8: Conservative
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nes 8; Conservative
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13 ilGCIVTSL 21
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           NCBI_TaxID-31647;
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                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-H05-4;
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                                                                                                                                                                                                                                                    Hepacivirus
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogata S.
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NON_TER
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Q8QVX3;
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Sest Local Similarity
8, Conserve
                                                                                                                        Genome polyprotein.
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                           NCBI_TaxID-11103;
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                                                                                                                                                                                                                                                  STRAIN=MD3-1
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                                 0901Y6;
0901Y6;
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RESULT 7
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1- SUBUNIT: THE VIRION OF THIS VIKUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MIND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
                                                                                                                                                                                                                                                           MEDLINE-20013325, PubMed-10544099,
Nagayama K., Kirosaki M., Encmoto N., Mackawa S.y., Kiyasaka Y.,
Tazawa J.i., Izumi N., Marumo F., Sato C., Arios and hepatitis
"Time-related changes in full-length lepatitis C virus and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane
SEQUENCE 3010 AA: 327436 MW; 1519023463DF8C35 CRC64;
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PROSITE; PS50521; RDRP_VIRAL; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
                                                                                                                                                        Viruses: ssRNA positive-strand viruses, no BNA stage: Blattviridae;
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                                                                                    Last sequence update)
Last annotation update)
                               3010 AA
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InterProj 1700 2531 HOV_NS2.
InterProj 1700 2548 HOV_NS3.
InterProj 1700 1049 HOV_NS3.
InterProj 1700 1049 HOV_NS4.
InterProj 1700 1049 HOV_NS4.
InterProj 1700 1049 HOV_NS5.
InterProj 1700 1049 HOV_NS5.
InterProj 1700 1049 HOV_NS5.
InterProj 1700 1049 HOV_Caps.
InterProj 1700 1049 HOV_Caps.
InterProj 1700 1049 HOV_Caps.
InterProj 1700 1049 HOV_NS2:
InterProj 1700 HOV_NS3:
InterProj 
                                                                   Created)
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HCV_core.
HCV_env.
HCV_NS:.
HCV_NS:.
HCV_NS:.
                                                               01-MAY-2000 (TrEMBLRG), 13,
01-MAY-2000 (TrEMBLRG), 13,
01-MAR-2003 (TrEMBLRG), 23,
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HSSP; P26663; lJXP.
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InterPro; IPR002522; HCV_c
InterPro; IPR002521; HCV_c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.9
Matches 8: Conservative
                               PRELIMINARY;
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InterPro; IPR002531;
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                                                                                                                        Genome polyprotein.
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-MD3-2;
                                                                                                                                         virus.
                                                                                                                                                                                                                           SEQUENCE PROM N.A.
                                                                                                                                                                                        NCBI_TaxID=11163;
                                                                                                                                                                                                                                                STRAIN=MD3-2;
                                                                                                                                                                       Hepacivirus
                              0901Y5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIRAINTHIDS-LISABLE AND LANGE AND MACKAWA S., Miyasaka Y., SARAINTHIDS-LISABLE AND LANGE AND LAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagayama K., Kurosaki M., Enomoto N., Maekawa S.y., Miyasaka Y.,
Tazawa J.i., Izumi N., Marumo F., Sato C.;
"Time-related changes in full-length hepatitis C virus and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS50507; RDRP_POS.TIVE; ...
PROSITE; PS50521; RDRP_VIRAL; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Rnv-directed RNA polymerase; Transferase; Transmembrane
                                                                                                                                                                                                                                   Hepatitis C'virus.
Viruses: sskNa positive-strand viruses, no DNA stage: Flaviviridae;
Hebacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indeis
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                                                                                   01-MAY-200C (TrEMBLrel, 13, Created)
01-MAY-200C (TrEMBLrel, 13, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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red, No. 12;
Mismatches 0;
PRT; 3010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20013325; PubMed-10544098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3010 AA: 327368 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Priam, PP01539; HCV_env; 1.
Priam, PP01560; HCV_NS; 1.
Priam, PP01540; HCV_NS; 1.
Priam, PP02907; HCV_NS3; 1.
Priam, PP01006; HCV_NS4b; 1.
Priam, PP01001; HCV_NS4b; 1.
Priam, PP01009; HCV_NS5b; 1.
Priam, PP01099; Viral_NS5b; 1.
Priam, PP01998; Viral_NSSP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virology 263:244-253(1999).
    PRELIM: NARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1039 LIGCIVISL 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM00487; DEXDC;
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01-WAR-2002 (TrEMBLrol. 20, Created) 01-WAR-2002 (TrEMBLrei. 20, Last sequence update) 01-WAR-2003 (TrEMBLrol. 23, Last annotation update)

3010 NA.

PRT;

PRELIMINARY:

Q8V638 Q8V638;

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RESUL,T
08V638
                                                SOLUTION OF THE PROPERTY OF TH
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                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PSS0507; RDRP_POSITIVE; 1.
PROSITE; PSS0521; RDRP_VIRAL: 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
POlyprotein; RNA-directed RNA polymerase; Iransferase; Iransmembrane,
SEQUENCE 3010 AA; 326595 MW; D186BA7E92F0B5E8 CRC64;
                                                                                                                                                                                                                                                              Nagayama K., Kurosaki M., Enomoto N., Maekawa S.y., Miyasuka Y.,
Tazawa J.i., Izumi N., Marumo F., Sato C.;
"Time-related changes in fuil-length hepatitis C virus and hepatitis
                                                                                                                                                 Virusos; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Length 3010;
                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43: DB 1
Pred. No. 12;
1; Mismatches
                                  3010 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20013325; PubMed-10544098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.78;
                                                                                                                                                                                                                                                                                                                             Virology 263:244-253(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR061410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.94
Seconservative 8, Conservative
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEXDC; 1
                                                                                                                  Genome polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THEI
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                   virus
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_Tax:D-11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00487;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MD5-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227958;
                                                                                                                                                                                                                                   STRAIN-MDS-1;
                                                                                                                                Hepatitis C
                                                                                                                                                                 Hepacivirus
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                                  Q9QIY2
 RESULT 8
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                                                                                                                                  Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane. SEQUENCE 3010 a. 327181 MW: 33AAAKCO7751CP10 CDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                               Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.7%; Score 43; DB 12; Length 3610; 88.9%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3010 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                      EMBL AF913916; AND MARK (BI STRILLING)

INTERPRO; IPRO0345; CytC_heme_bind.

INTERPRO; IPRO0345; CytC_heme_bind.

INTERPRO; IPRO02521; HCV_core.

INTERPRO; IPRO02521; HCV_core.

INTERPRO; IPRO02531; HCV_RS1.

INTERPRO; IPRO02518; HCV_RS1.

INTERPRO; IPRO03518; HCV_RS2.

INTERPRO; IPRO03409; HCV_RS3.

INTERPRO; IPRO03490; HCV_RS3.

INTERPRO; IPRO03490; HCV_RS4.

INTERPRO; IPRO03490; HCV_RS4.

INTERPRO; IPRO03686; HCV_RS4.

INTERPRO; IPRO03686; HCV_RS4.

INTERPRO; IPRO03686; HCV_RS4.

INTERPRO; IPRO03686; HCV_RS4.

INTERPRO; IPRO07094; HNA_POL_PSVIT.

Pfam: PF01542; HCV_core: I.

Pfam: PF01542; HCV_core: I.

Pfam: PF01556; HCV_LOS?: I.

Pfam: PF01556; HCV_LOS?: I.

Pfam: PF01556; HCV_LOS?: I.

Pfam: PF01556; HCV_LOS?: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS0019C; CYTOCHROME_C: 1. PROSITE: PS50507; RDRP_POSITIVE; 1. PROSITE: PS50521; RDRP_VIRAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fiam; PF01006; HCV_NS44; 1. Pfam; PF01001; HCV_NS4b; 1. Pfam; PF01506; HCV_NS54; 1. Ptam; PF00998; Viral_RGRP; 1. Pr0Dom; PD18665; HCV_NS; 1. SMART; SM00487; DEXDC; 1.
Genome polyprotein (Fragment). Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01,
01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 88.9
Second By Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              081541;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1039 LEGCIVISE 1047
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                                                                                                                    SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=11103;
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Q81541
ID Q8154:
AC Q8154:
DT 01-NOV
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Gaps

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ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase; Hydroclase; Nonstructural protein; Polyprotein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane. SEGUENCE 3010 AA: 327108 MR: DE182D810EF78E54 CRC64;
                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                  Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.,
Hatahara I., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                     01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3011 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LITERPOZDE9; HCV_NS4a.
LITERPOZDE9; HCV_NS4b.
LITERPOZDE6; HCV_RGAB.
TILERPOZDE TERROZDE6; HCV_RGAB.
TILERPOZDE TERROZDE6; HCV_RGAB.
TILERPOZDE TERROZDE6; HCV_RGAB.
FRAM: PF01543; HCV_CORF.
Pfam: PF01542; HCV_CORF.
Pfam: PF01542; HCV_CORF.
TGAM: PF01560; HCV_NS1; 1.
Sam: PF01560; HCV_NS1; 1.
Sam: PF01560; HCV_NS2; 1.
TERROZDESSE TERROZDESSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.7%; Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS50507; RDRP_POSITIVE; 1.
PROSITE; PS50521: RDRP_VIRAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::terPro; IPR006345; CytC_heme_bind
::terPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
InterPro; IPR002531; HCV_env.
InterPro; IPR002531; HCV_NSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF02907; HCV_NS3; ::
PF01006; HCV_NS4s: 1.
PF01506; HCV_NS4b: 1.
PF01506; HCV_NS5a: 1.
PF01506; HCV_NS5a: 1.
PF00991; NellCase_C: 1.
PF00998; Varal_RdRF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HCV_NS2.
HCV_NS3.
HCV_NS4a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: AB049101; BAB18814.1;
HSSP; P26663; lJXP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1039 LLGCIVTSL 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRC04109; H
InterPro; IPR000745; H
InterPro; IPR001490; H
InterPro; IPR002869; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEXDC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR0C2519;
InterPro, IPR0C2531;
InterPro, IPR0C2518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LLGCIITSL 9
                                                                                                                 Genome polyprotein.
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
tes 8; Conserv
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID-11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00487;
                                                                                                                                                                                                           Repacivirus
                                                                                                                                                                                                                                                                                                                                                                                                             Mishiro S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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SMART: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0913D4
0913D4:
09DIDE)
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Pfam;
Pfam;
Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2913D4
ID 09
5
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                                                                                                                                                                                                                                                                                              Tanaka T., Kato N., Nakagawa M., Ootsuyamu Y., Cho M.J., Nakazawa I., Hijikata M., Ishimura Y., Shimotohno K.; "Molecular cioning of hepatitis C virus genome from a single Japanese Carrier: sequence variation within the same individual and among infected individuals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; PD186va, ...
SMART; SM0487; DEXDC; ;
PROSTE; PS5507; RDRP_POSITIVE; 1,
PROSTE; PS5507; RDRP_POSITIVE; 1,
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; HNA-directed RNA polymeraso; Transferaso; Transmembrano, CHAIN 191 PUT, GP3.
CHAIN 192 PUT, GP70.
CHAIN 384 729 PUT, GP70.
The coat of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Virus Res. 23:39-53(1992).
-i- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLECCAPSID COVERED BY A LIPOPROFILE ENVELOPE CONSISTS OF TWO PROTEINS:
PROFILE MENULUM GANCOPERINE: THE NUCLECCAPSID IS A SCHPLEN OF PROTEIN OF AND NEWA (SY SIMILARITY).
                        Genome polyprotein.
Hepatitis C virus.
Viruses: ssRNA positive-strand viruses. no DNA stage: Flaviviridae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trdels
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23, Last annotation update)
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Interpro: IPR007094; RNA_pol_PSvir.
Pfam; PF01543; HCV_capsid; l.
Pfam; PF01542; HCV_core; ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001410; DRAD.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002522; HCV_cape.
InterPro; IPR002519; HCV_env.
InterPro; IPR002519; HCV_RSI.
InterPro; IPR002518; HCV_RSI.
                                                                                                                                                                                                                                                               MEDLINE-92295714; PubMed-1318627:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR002531; HCV_NS1.
InterPro; IPR002518; HCV_NS2.
InterPro; IPR004109; HCV_NS3.
InterPro; IPR000145; HCV_NS4a.
InterPro; IPR002868; HCV_NS4b.
InterPro; IPR002868; HCV_NS5a.
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Probom; PD186062; HCV_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF01566) HCV_NS1; 1.
PF01538; HCV_NS2; 1.
PF01006; HCV_NS4a; 1.
PF01001; HCV_NS4a; 1.
PF01506; HCV_NS5a; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D11355; BAA18894.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 88.9
Nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1039 LIGGIVISL 1047
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                             NCBI_TaxID-11103;
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1963
2014
3010
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HSSP; P26663;
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Pfam; Pfam; Pfam; Pfam;

Pfam;

Pfam;

Ptam;

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Gaps

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RESULT 11 09DTD6 £

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Naqayama K., Kurosaki M., Endmoto N., Miyasaka Y., Marumo F., Sato C.;
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Submarted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIRUMIT: THE VIRION OF THIS VIRUS IS A NUCLECCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN B. THE NUCLECCAPSID IS A COMPLEX OF PROTEIN C AND MRNA (BY SIMILARITY).
HMBL: AF207754; AARF55944.1; --
HSSF: P26663; 1JXP.
                                                                                                                                   Holland-Staley C.A., Kovari L.C., Golenborg E., Mayers D.L.;
"Genetic Diversity and response to IFN of the NS3 Protease Gene from
Clinical Strains of the Hepatitis C Virus.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF369258; AAK54583.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characteristics of hepatitis C viral genome associated with disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses: ssRNA positive-strand viruses, no DNA stage: Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 12; Length 181;
Pred. No. 1.8;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           19056 MW; BAF89690AD2971DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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InterPro; IPR001490; HCV_N84b.
InterPro; IPR001868; HCV_N85b.
InterPro; IPR00166; HCV_RGRP.
InterPro; IPR001095; RNA_DOL_DS_PS.
InterPro; IPR007095; RNA_DOL_PSvir.
Pfam: PF01143; HCV_capsid; 1.
Pfam: PF011442; HCV_capsid; 1.
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InterPro: IPR001410; DEAD.
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Interpro; IPR002521; HCV_core.
Interpro; IPR002519; HCV_env.
Interpro; IPR002531; HCV_NS1.
Interpro; IPR004109; HCV_NS3.
                                                                                                                                                                                                                                                                   MEROPS; S29.001; -...
MEROFS; U39.001; -..
InterPro; IPR004109; HCV_NS3.
Prontesse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 88.9
8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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181 AA;
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                                                                                      SEQUENCE FROM N.A.
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        Hepacivitus.
NCBI_TaxID=11103;
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                                                                                                               STRAIN-Pt.30
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SEQUENCE
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Best Loca: S
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Pfam;
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Q9J3H9
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                                                                                                                                                                                                                                                                   Guntaka R.V., Wunpally S.K., Khaja M.N., Kota K.K., Ramana V.K.,
Swaminathan S., Sakata Y., Habebullah C.M.;
Swaminathan S., Sakata Y., Habebullah C.M.;
"Nucleotide Sequence of Indian strain of Hepa: tiss C Virus.";
submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- SQBUNT: THE VIRION OF THIS VIRUS IS A NUCLEOSAFSID COVERED BY
LIPOPROTEIN WHO GINCOPROTEIN E. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GINCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
EMBL: ANOSI292; AMA95832.1: -.
MERROS; $29.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00190; CYTGGHROME,C: 1.
PROSITE; PS50507; RDRP_POS_TIVE; 1.
PROSITE; PS50507; RDRP_VIRAL; 1.
Coat protein; Envelope protein; Glycoprotein; Monstructural protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA-directed RNA polymerase, Transferase, Transmembrane
011 AA: 327234 MW: 57A2196484227860 CR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .:
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
NS3 proclease (Fragment).
                           01-DEC-2001 (TrEMBLrel. 19. Last sequence update)
01-MAR-2003 (TrEMBLrel. 23. Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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01-DEC-2001 (TrEMBLrel, 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 88.3%,
Best Local Similarity 88.3%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                      Genome polyprotein.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                        NCBL_TaxID-11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; U39.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polyprotein:
SEQUENCE 30
                                                                                                                  Hepatitis C
                                                                                                                                                                 Hepacivirus
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PROSTIE: PRO0139; CTTCCHROME_C: 1.
PROSTIE: PS50507; BDRP_POSTITVE; 1.
PROSTIE: PS50521; RDHP_VIRAL: 1.
Coat protein: Rivelope protein; Glycoprotein; Nonstructural protein;
PPOlyprotein: NNA-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3010 AA: 32694 MW; AF12CCGGGGAHBOTE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses, ssRNA positive-strand viruses, no DNA staqe, Flaviviridae;
Hepacivirus,
                                                                                                                                                                                                                                                                                                                            95.5%; Score 42; UB 12; Length 3010;
86.9%; Pred. No. 19;
179. 1: Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TFEMBLIEL. 15, Created)
01-0CT-2000 (TFEMBLIEL. 15, Last sequence update)
01-0CT-2000 (TFEMBLIEL. 23, Last annotation update)
Genome polyprotein.
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT: 3316 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPR007095; RNA_pol_DS_PS.
InterPro: IPR007094; RNA_pol_DSvir.
Pfam. PF01543; HCV_capsid: 1
Pfam: PF01542; HCV_core; 1
                              Pfam: PFC1006; HCV_NS4a; 1.
Pfam: PPC1001; HCV_NS4b: 1.
Pfam: PFC1001; HCV_NS5a: 1.
Pfam: PF00999; Viral_RG4P; 1.
Probom: PD:86562; HCV_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00271; helicase_C: 1.
PF00998; Viral_RdRP: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCV_NS4a;
HCV_NS4b;
HCV_NS5a;
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 86.9
Matches 8: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF01542; HCV_core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1039 MIGCILTSL 1047
                                                                                                                                                                                                                                                                                                                                                                                                                    1 LIGGIITSE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF01560; PF01538; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF02907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-MD27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
Pfam;
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DR Probom; PD186062; HCV_NSI; 1.

DR SMART; SMO0487; DEXDC: 1.

DR PROSITE: PS00190; CYTOCHROME_C; 2.

DR PROSITE: PS50507; RDPR_POSTTVE; i.

DR PROSITE: PS5051; RDPR_VIRAL; 1.

MW ATP-binding, Coat protein; Envelope protein; Glycoprotein; Helicase:

KW ATP-binding Coat protein; Envelope protein; Helicase:

KW HYdrolase; Nonstructural protein; Polyprotein;

KW RNA-directed RNA polymerase; Transferase; Transmembrane.

SO SEQUENCE 30:0 AA: 327:77 MW; 47A31DD7678DE62F CRC64;

Outry Match

SOS SEQUENCE 30:0 AA: 327:77 MW; 47A31DD7678DE62F CRC64;

Outry Match

SOS SEQUENCE 30:0 AA: 327:77 MW; 47A31DD7678DE62F CRC64;

Outry Match

SOS SEQUENCE 30:0 AA: 327:77 MW; 47A31DD7678DE62F CRC64;

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SOS SEQUENCE 30:0 AA: 327:77 MW; 47A31DD7678DE62F CRC64;

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Outry MATCH

SOS SEQUENCE 30:0 AA: 327:77 MW; 47A31DD7678DE62F CRC64;

Outry MATCH

SOS SEQUENCE 30:0 AA: 327:77 MM; 47A31DD7678DE62F CRC64;

Outry MATCH

SOS SEQUENCE 30:0 AA: 327:77 MM; 47A31DD7678DE62F CRC64;

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Search completed: September 29, 2003, 19:08:26 Job time : 32 secs